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Application for U.S. Letters Patent Entitled

POSITION DEPENDENT RECOGNITION OF GNN
NUCLEOTIDE TRIPLETS BY ZINC FINGERS

which is a continuation-in-part of copending U.S. Patent Application Serial No. 09/535,008, filed March 23, 2000, which application claims the benefit of U.S. provisional applications 60/126,238, filed March 24, 1999, 60/126,239, filed March 24, 1999, 60/146,595, filed July 30, 1999 and 60/146,615, filed July 30, 1999. The present application is also a continuation-in-part of copending U.S. Patent Application Serial No. 09/716,637, filed November 20, 2000.

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POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE TRIPLETS BY ZINC FINGERS

CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is a continuation-in-part of copending U.S. Patent Application Serial No. 09/535,008, filed March 23, 2000, which application claims the benefit of U.S. provisional applications 60/126,238, filed March 24, 1999, 60/126,239 filed March 24, 1999, 60/146,595 filed July 30, 1999 and 60/146,615 filed July 30, 1999.

The present application is also a continuation-in-part of copending U.S. Patent Application Serial No. 09/716,637, filed November 20, 2000. The disclosures of all of the aforementioned applications are hereby incorporated by reference in their entireties for all purposes.

BACKGROUND

Zinc finger proteins (ZFPs) are proteins that can bind to DNA in a sequence-specific manner. Zinc fingers were first identified in the transcription factor TFIIIA from the oocytes of the African clawed toad, *Xenopus laevis*. An exemplary motif characterizing one class of these protein (C_2H_2 class) is -Cys-(X)₂₋₄-Cys-(X)₁₂-His-(X)₃₋₅-His (where X is any amino acid) (SEQ. ID. No:1). A single finger domain is about 30 amino acids in length, and several structural studies have demonstrated that it contains an alpha helix containing the two invariant histidine residues and two invariant cysteine residues in a beta turn co-ordinated through zinc. To date, over 10,000 zinc finger sequences have been identified in several thousand known or putative transcription factors. Zinc finger domains are involved not only in DNA-recognition, but also in RNA binding and in protein-protein binding. Current estimates are that this class of molecules will constitute about 2% of all human genes.

The x-ray crystal structure of Zif268, a three-finger domain from a murine transcription factor, has been solved in complex with a cognate DNA sequence and shows that each finger can be superimposed on the next by a periodic rotation. The structure suggests that each finger interacts independently with DNA over 3 base-pair

intervals, with side-chains at positions -1, 2, 3 and 6 on each recognition helix making contacts with their respective DNA triplet subsites. The amino terminus of Zif268 is situated at the 3' end of the DNA strand with which it makes most contacts. Some zinc fingers can bind to a fourth base in a target segment. If the strand with which a zinc finger protein makes most contacts is designated the target strand, some zinc finger proteins bind to a three base triplet in the target strand and a fourth base on the nontarget strand. The fourth base is complementary to the base immediately 3' of the three base subsite.

The structure of the Zif268-DNA complex also suggested that the DNA sequence specificity of a zinc finger protein might be altered by making amino acid substitutions at the four helix positions (-1, 2, 3 and 6) on each of the zinc finger recognition helices. Phage display experiments using zinc finger combinatorial libraries to test this observation were published in a series of papers in 1994 (Rebar et al., *Science* 263, 671-673 (1994); Jamieson et al., *Biochemistry* 33, 5689-5695 (1994); Choo et al, *PNAS* 91, 11163-11167 (1994)). Combinatorial libraries were constructed with randomized side-chains in either the first or middle finger of Zif268 and then used to select for an altered Zif268 binding site in which the appropriate DNA sub-site was replaced by an altered DNA triplet. Further, correlation between the nature of introduced mutations and the resulting alteration in binding specificity gave rise to a partial set of substitution rules for design of ZFPs with altered binding specificity.

Greisman & Pabo, *Science* 275, 657-661 (1997) discuss an elaboration of the phage display method in which each finger of a Zif268 was successively randomized and selected for binding to a new triplet sequence. This paper reported selection of ZFPs for a nuclear hormone response element, a p53 target site and a TATA box sequence.

A number of papers have reported attempts to produce ZFPs to modulate particular target sites. For example, Choo et al., *Nature* 372, 645 (1994), report an attempt to design a ZFP that would repress expression of a bcr-abl oncogene. The target segment to which the ZFPs would bind was a nine base sequence 5'GCA GAA GCC3' chosen to overlap the junction created by a specific oncogenic translocation fusing the genes encoding bcr and abl. The intention was that a ZFP specific to this target site would bind to the oncogene without binding to abl or bcr component genes. The authors

used phage display to screen a mini-library of variant ZFPs for binding to this target segment. A variant ZFP thus isolated was then reported to repress expression of a stably transfected bcr-able construct in a cell line.

Pomerantz et al., *Science* 267, 93-96 (1995) reported an attempt to design a novel DNA binding protein by fusing two fingers from Zif268 with a homeodomain from Oct-1. The hybrid protein was then fused with a transcriptional activator for expression as a chimeric protein. The chimeric protein was reported to bind a target site representing a hybrid of the subsites of its two components. The authors then constructed a reporter vector containing a luciferase gene operably linked to a promoter and a hybrid site for the chimeric DNA binding protein in proximity to the promoter. The authors reported that their chimeric DNA binding protein could activate expression of the luciferase gene.

Liu et al., *PNAS* 94, 5525-5530 (1997) report forming a composite zinc finger protein by using a peptide spacer to link two component zinc finger proteins each having three fingers. The composite protein was then further linked to transcriptional activation domain. It was reported that the resulting chimeric protein bound to a target site formed from the target segments bound by the two component zinc finger proteins. It was further reported that the chimeric zinc finger protein could activate transcription of a reporter gene when its target site was inserted into a reporter plasmid in proximity to a promoter operably linked to the reporter.

Choo et al., WO 98/53058, WO98/53059, and WO 98/53060 (1998) discuss selection of zinc finger proteins to bind to a target site within the HIV Tat gene. Choo et al. also discuss selection of a zinc finger protein to bind to a target site encompassing a site of a common mutation in the oncogene ras. The target site within ras was thus constrained by the position of the mutation.

Previously-disclosed methods for the design of sequence-specific zinc finger proteins have often been based on modularity of individual zinc fingers; *i.e.*, the ability of a zinc finger to recognize the same target subsite regardless of the location of the finger in a multi-finger protein. Although, in many instances, a zinc finger retains the same sequence specificity regardless of its location within a multi-finger protein; in certain cases, the sequence specificity of a zinc finger depends on its position. For example, it is possible for a finger to recognize a particular triplet sequence when it is

present as finger 1 of a three-finger protein, but to recognize a different triplet sequence when present as finger 2 of a three-finger protein.

Attempts to address situations in which a zinc finger behaves in a non-modular fashion (*i.e.*, its sequence specificity depends upon its location in a multi-finger protein) have, to date, involved strategies employing randomization of key binding residues in multiple adjacent zinc fingers, followed by selection. *See*, for example, Isalan *et al.* (2001) *Nature Biotechnol.* **19**:656-660. However, methods for rational design of polypeptides containing non-modular zinc fingers have not heretofore been described.

SUMMARY

The present disclosure provides compositions comprising and methods involving position dependent recognition of GNN nucleotide triplets by zinc fingers.

Thus, provided herein is a zinc finger protein that binds to a target site, said zinc finger protein comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, said target site comprising, in 3' to 5' direction, a first (S1), a second (S2), and a third (S3) target subsite, each target subsite having the nucleotide sequence GNN, wherein if S1 comprises GAA, F1 comprises the amino acid sequence QRSNLVR; if S2 comprises GAA, F2 comprises the amino acid sequence QSGNLAR; if S3 comprises GAA, F3 comprises the amino acid sequence QSGNLAR; if S1 comprises GAG, F1 comprises the amino acid sequence RSDNLAR; if S2 comprises GAG, F2 comprises the amino acid sequence RSDNLAR; if S3 comprises GAG, F3 comprises the amino acid sequence RSDNLTR; if S1 comprises GAC, F1 comprises the amino acid sequence DRSNLTR; if S2 comprises GAC, F2 comprises the amino acid sequence DRSNLTR; if S3 comprises GAC, F3 comprises the amino acid sequence DRSNLTR; if S1 comprises GAT, F1 comprises the amino acid sequence QSSNLAR; if S2 comprises GAT, F2 comprises the amino acid sequence TSGNLVR; if S3 comprises GAT, F3 comprises the amino acid sequence TSANLSR; if S1 comprises GGA, F1 comprises the amino acid sequence QSGHLAR; if S2 comprises GGA, F2 comprises the amino acid sequence QSGHLQR; if S3 comprises GGA, F3 comprises the amino acid sequence QSGHLQR; if S1 comprises GGG, F1 comprises the amino acid sequence RSDHLAR; if S2 comprises GGG, F2 comprises the amino acid sequence

RSDHLSR; if S3 comprises GGG, F3 comprises the amino acid sequence RSDHLSR; if S1 comprises GGC, F1 comprises the amino acid sequence DRSHLRT; if S2 comprises GGC, F2 comprises the amino acid sequence DRSHLAR; if S1 comprises GGT, F1 comprises the amino acid sequence QSSHLTR; if S2 comprises GGT, F2 comprises the amino acid sequence TSGHLSR; if S3 comprises GGT, F3 comprises the amino acid sequence TSGHLVR; if S1 comprises GCA, F1 comprises the amino acid sequence QSGSLTR; if S2 comprises GCA, F2 comprises QSGDLTR; if S3 comprises GCA, F3 comprises QSGDLTR; if S1 comprises GCG, F1 comprises the amino acid sequence RSDDLTR; if S2 comprises GCG, F2 comprises the amino acid sequence RSDDLQR; if S3 comprises GCG, F3 comprises the amino acid sequence RSDDLTR; if S1 comprises GCC, F1 comprises the amino acid sequence ERGTLAR; if S2 comprises GCC, F2 comprises the amino acid sequence DRSDLTR; if S3 comprises GCC, F3 comprises the amino acid sequence DRSDLTR; if S1 comprises GCT, F1 comprises the amino acid sequence QSSDLTR; if S2 comprises GCT, F2 comprises the amino acid sequence QSSDLTR; if S3 comprises GCT, F3 comprises the amino acid sequence QSSDLQR; if S1 comprises GTA, F1 comprises the amino acid sequence QSGALTR; if S2 comprises GTA, F2 comprises the amino acid sequence QSGALAR; if S1 comprises GTG, F1 comprises the amino acid sequence RSDALTR; if S2 comprises GTG, F2 comprises the amino acid sequence RSDALSR; if S3 comprises GTG, F3 comprises the amino acid sequence RSDALTR; if S1 comprises GTC, F1 comprises the amino acid sequence DRSEALAR; if S2 comprises GTC, F2 comprises the amino acid sequence DRSEALAR; and if S3 comprises GTC, F3 comprises the amino acid sequence DRSEALAR.

Also provided are methods of designing a zinc finger protein comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus that binds to a target site comprising, in 3' to 5' direction, a first (S1), a second (S2), and a third (S3) target subsite, each target subsite having the nucleotide sequence GNN, the method comprising the steps of (a) selecting the F1 zinc finger such that it binds to the S1 target subsite, wherein if S1 comprises GAA, F1 comprises the amino acid sequence QRSNLVR; if S1 comprises GAG, F1 comprises the amino acid sequence RSDNLAR; if S1 comprises GAC, F1 comprises the amino acid sequence DRSNLTR; if S1 comprises GAT, F1 comprises the amino acid sequence QSSNLAR; if

S1 comprises GGA, F1 comprises the amino acid sequence QSGHLAR; if S1 comprises GGG, F1 comprises the amino acid sequence RSDHLAR; if S1 comprises GGC, F1 comprises the amino acid sequence DRSHLRT; if S1 comprises GGT, F1 comprises the amino acid sequence QSSHLTR; if S1 comprises GCA, F1 comprises QSGSLTR; if S1
5 comprises GCG, F1 comprises RSDDLTR; if S2 comprises GCG, F2 comprises RSDDLQR; if S1 comprises GCC, F1 comprises ERGTLAR; if S1 comprises GCT, F1 comprises the amino acid sequence QSSDLTR; if S1 comprises GTA, F1 comprises the amino acid sequence QSGALTR; if S1 comprises GTG, F1 comprises the amino acid sequence RSDALTR; if S1 comprises GTC, F1 comprises the amino acid sequence
10 DRSLAR; (b) selecting the F2 zinc finger such that it binds to the S2 target subsite, wherein S2 comprises GAA, F2 comprises the amino acid sequence QSGNLR; if S2 comprises GAG, F2 comprises the amino acid sequence RSDNLR; if S2 comprises GAC, F2 comprises the amino acid sequence DRSNLTR; if S2 comprises GAT, F2 comprises the amino acid sequence TSGNLVR; if S2 comprises GGA, F2 comprises the amino acid sequence QSGHLQR; if S2 comprises GGG, F2 comprises the amino acid sequence RSDHLR; if S2 comprises GGC, F2 comprises the amino acid sequence DRSHLAR; if S2 comprises GGT, F2 comprises the amino acid sequence TSGHLR; if S2 comprises GCA, F2 comprises the amino acid sequence QSGDLTR; if S2 comprises GCC, F2 comprises the amino acid sequence DRSDLTR; if S2 comprises GCT, F2
20 comprises the amino acid sequence QSSDLTR; if S2 comprises GTA, F2 comprises the amino acid sequence QSGALAR; if S2 comprises GTG, F2 comprises the amino acid sequence RSDALR; if S2 comprises GTC, F2 comprises the amino acid sequence DRSLAR; and (c) selecting the F3 zinc finger such that it binds to the S3 target subsite, wherein if S3 comprises GAA, F3 comprises the amino acid sequence QSGNLR; if S3
25 comprises GAG, F3 comprises the amino acid sequence RSDNLTR; if S3 comprises GAC, F3 comprises the amino acid sequence DRSNLTR; if S3 comprises GAT, F3 comprises the amino acid sequence TSANLVR; if S3 comprises GGA, F3 comprises the amino acid sequence QSGHLQR; if S3 comprises GGG, F3 comprises RSDHLR; if S3 comprises GGT, F3 comprises the amino acid sequence TSGHLVR; if S3 comprises GCA, F3 comprises the amino acid sequence QSGDLTR; if S3 comprises GCG, F3
30 comprises the amino acid sequence RSDDLTR; if S3 comprises GCC, F3 comprises the

amino acid sequence DRSDLTR; if S3 comprises GCT, F3 comprises the amino acid sequence QSSDLQR; if S3 comprises GTG, F3 comprises RSDALTR; and if S3 comprises GTC, F3 comprises the amino acid sequence DRSALAR;

thereby designing a zinc finger protein that binds to a target site.

5 In certain embodiments of the zinc finger proteins and methods described herein, S1 comprises GAA and F1 comprises the amino acid sequence QRSNLVR. In other embodiments, S2 comprises GAA and F2 comprises the amino acid sequence QSGNLAR. In other embodiments, S3 comprises GAA and F3 comprises the amino acid sequence QSGNLAR. In other embodiments, S1 comprises GAG and F1 comprises the amino acid sequence RSDNLAR. In other embodiments, S2 comprises GAG and F2 comprises the amino acid sequence RSDNLAR. In other embodiments, S3 comprises GAG and F3 comprises the amino acid sequence RSDNLTR. In other embodiments, S1 comprises GAC and F1 comprises the amino acid sequence DRSNLTR. In other embodiments, S2 comprises GAC and F2 comprises the amino acid sequence DRSNLTR. In other embodiments, S3 comprises GAC and F3 comprises the amino acid sequence DRSNLTR. In other embodiments, S1 comprises GAT and F1 comprises the amino acid sequence QSSNLAR. In other embodiments, S2 comprises GAT and F2 comprises the amino acid sequence TSGNLVR. In other embodiments, S3 comprises GAT and F3 comprises the amino acid sequence TSANLSR. In other embodiments, S1 comprises GGA and F1 comprises the amino acid sequence QSGHLAR. In other embodiments, S2 comprises GGA and F2 comprises the amino acid sequence QSGHLQR. In other embodiments, S3 comprises GGA and F3 comprises the amino acid sequence QSGHLQR. In other embodiments, S1 comprises GGG and F1 comprises the amino acid sequence RSDHLAR. In other embodiments, S2 comprises GGG and F2 comprises the amino acid sequence RSDHLSR. In other embodiments, S3 comprises GGG and F3 comprises the amino acid sequence RSDHLSR. In other embodiments, S1 comprises GGC and F1 comprises the amino acid sequence DRSHLTR. In other embodiments, S2 comprises GGC and F2 comprises the amino acid sequence DRSHLAR. In other embodiments, S1 comprises GGT and F1 comprises the amino acid sequence QSSHLTR. In other embodiments, S2 comprises GGT and F2 comprises the amino acid sequence TSGHLSR. In other embodiments, S3 comprises GGT and F3

comprises the amino acid sequence TSGHLVR. In other embodiments, S1 comprises GCA and F1 comprises the amino acid sequence QSGSLTR. In other embodiments, S2 comprises GCA and F2 comprises the amino acid sequence QSGDLTR. In other embodiments, S3 comprises GCA and F3 comprises the amino acid sequence QSGDLTR. In other embodiments, S1 comprises GCG and F1 comprises the amino acid sequence RSDDLTR. In other embodiments, S2 comprises GCG and F2 comprises the amino acid sequence RSDDLQR. In other embodiments, S3 comprises GCG and F3 comprises the amino acid sequence RSDDLTR. In other embodiments, S1 comprises GCC and F1 comprises the amino acid sequence ERGTLAR. In other embodiments, S2 comprises GCC and F2 comprises the amino acid sequence DRSDLTR. In other embodiments, S3 comprises GCC and F3 comprises the amino acid sequence DRSDLTR. In other embodiments, S1 comprises GCT and F1 comprises the amino acid sequence QSSDLTR. In other embodiments, S2 comprises GCT and F2 comprises the amino acid sequence QSSDLTR. In other embodiments, S3 comprises GCT and F3 comprises the amino acid sequence QSSDLQR. In other embodiments, S1 comprises GTA and F1 comprises the amino acid sequence QSGALTR. In other embodiments, S2 comprises GTA and F2 comprises the amino acid sequence QSGALAR. In other embodiments, S1 comprises GTG and F1 comprises the amino acid sequence RSDALTR. In other embodiments, S2 comprises GTG and F2 comprises the amino acid sequence RSDALSR. In other embodiments, S3 comprises GTG and F3 comprises the amino acid sequence RSDALTR. In other embodiments, S1 comprises GTC and F1 comprises the amino acid sequence DRSALAR. In other embodiments, S2 comprises GTC and F2 comprises the amino acid sequence DRSALAR. In other embodiments, S3 comprises GTC and F3 comprises the amino acid sequence DRSALAR.

Also provided are polypeptides comprising any of zinc finger proteins described herein. In certain embodiments, the polypeptide further comprises at least one functional domain. Also provided are polynucleotides encoding any of the polypeptides described herein. Thus, also provided are nucleic acid encoding zinc fingers, including all of the zinc fingers described above.

Also provided are segments of a zinc finger comprising a sequence of seven contiguous amino acids as shown herein. Also provided are nucleic acids encoding any of these segments and zinc fingers comprising the same.

Also provided are zinc finger proteins comprising first, second and third zinc fingers. The first, second and third zinc fingers comprise respectively first, second and third segments of seven contiguous amino acids as shown herein. Also provided are nucleic acids encoding such zinc finger proteins.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows results of site selection analysis of two representative zinc finger proteins (leftmost 4 columns) and measurements of binding affinity for each of these proteins to their intended target sequences and to variant target sequences. (rightmost 3 columns). Analysis of ZFP1 is shown in the upper portion of the figure and analysis of ZFP2 is shown in the lower portion of the figure. For the site selection analyses, the amino acid sequences of residues -1 through +6 of the recognition helix of each of the three component zinc fingers (F3, F2 and F1) are shown across the top row; the intended target sequence (divided into finger-specific target subsites) is shown across the second row, and a summary of the sequences bound is shown in the third row. Data for F3 is shown in the second column, data for F2 is shown in the third column, and data for F1 is shown in the third column.

For the binding affinity analyses, the designed target sequence for each ZFP ("cognate") and two related sequences ("Mt") are shown (column 6), along with the K_d for binding of the ZFP to each of these sequences (column 7).

Figure 2 shows amino acid sequences of zinc finger recognition regions (amino acids -1 through +6 of the recognition helix) that bind to each of the 16 GNN triplet subsites. Three amino acid sequences are shown for each trinucleotide subsite; these correspond to optimal amino acid sequences for recognition of the subsite from each of the three positions (finger 1, F1; finger 2, F2; or finger 3, F3) in a three-finger zinc finger protein. Amino acid sequences are from N-terminal to C-terminal; nucleotide sequences are from 5' to 3'.

Also shown are site selection results for each of the 48 position-dependent GNN-recognizing zinc fingers. These show the number of times a particular nucleotide was present, at a given position, in a collection of oligonucleotide sequences bound by the finger. For example, out of 15 oligonucleotides bound by a zinc finger protein with the amino acid sequence QSGHLAR present at the finger 1 (F1) position, 15 contained a G in the 5'-most position of the subsite, 15 contained a G in the middle position of the subsite, while, at the 3'-most position of the subsite, 10 contained an A, 3 contained a G and 2 contained a T. Accordingly, this particular amino acid sequence is optimal for binding a GGA triplet from the F1 position.

Figures 3A, 3B and 3C show site selection data indicating positional dependence of GCA-, GAT- and GGT-binding zinc fingers. The first and fourth (where applicable) rows of each figure show portions of the amino acid sequence of a designed zinc finger protein. Amino acid residues-1 through +6 of each α -helix are listed from left to right. The second and fifth (where applicable) rows show the target sequence, divided into three triplet subsites, one for each finger of the protein shown in the first and fourth (where applicable) rows, respectively. The third and sixth (where applicable) rows show the distribution of nucleotides in the oligonucleotides obtained by site selection with the proteins shown in the first and fourth (where applicable) rows, respectively. Figure 3A shows data for fingers designed to bind GCA; Figure 3B shows data for fingers designed to bind GAT; Figure 3C shows data for fingers designed to bind GGT.

Figures 4A and 4B show properties of the engineered ZFP EP2C. Figure 4A shows site selection data. The first row provides the amino acid sequences of residues -1 through +6 of the recognition helices for each of the three zinc fingers of the EP2C protein. The second row shows the target sequence (5' to 3'); with the distribution of nucleotides in the oligonucleotides obtained by site selection indicated below the target sequence.

Figure 4B shows *in vitro* and *in vivo* assays for the binding specificity of EP2C. The first three columns show *in vitro* measurements of binding affinity of EP2C to its intended target sequence and several related sequences. The first column gives the name of each sequence (2C0 is the intended target sequence, compare to Figure 4A). The second column shows the nucleotide sequence of various target sequences, with

differences from the intended target sequence (2C0) highlighted. The third column shows the K_d (in nM) for binding of EP2C to each of the target sequences. K_d s were determined by gel shift assays, using 2-fold dilution series of EP2C. The right side of the figure (fourth column and bar graph) shows relative luciferase activities (normalized to β -galactosidase levels) in stable cell lines in which expression of EP2C is inducible. Cells were co-transfected with a vector containing a luciferase coding region under the transcriptional control of the target sequence shown in the same row of the figure, and a control vector encoding β -galactosidase. Luciferase and β -galactosidase levels were measured after induction of EP2C expression. Triplicate samples were assayed and the standard deviations are shown in the bar graph. pGL3 is a luciferase-encoding vector lacking EP2C target sequences. 3B is another negative control, in which luciferase expression is under transcriptional control of sequences (3B) unrelated to the EP2C target sequence.

DEFINITIONS

A zinc finger DNA binding protein is a protein or segment within a larger protein that binds DNA in a sequence-specific manner as a result of stabilization of protein structure through coordination of a zinc ion. The term zinc finger DNA binding protein is often abbreviated as zinc finger protein or ZFP.

Zinc finger proteins can be engineered to recognize a selected target sequence in a nucleic acid. Any method known in the art or disclosed herein can be used to construct an engineered zinc finger protein or a nucleic acid encoding an engineered zinc finger protein. These include, but are not limited to, rational design, selection methods (*e.g.*, phage display) random mutagenesis, combinatorial libraries, computer design, affinity selection, use of databases matching zinc finger amino acid sequences with target subsite nucleotide sequences, cloning from cDNA and/or genomic libraries, and synthetic constructions. An engineered zinc finger protein can comprise a new combination of naturally-occurring zinc finger sequences. Methods for engineering zinc finger proteins are disclosed in co-owned WO 00/41566 and WO 00/42219; as well as in WO 98/53057; WO 98/53058; WO 98/53059 and WO 98/53060; the disclosures of which are hereby incorporated by reference in their entireties. Methods for identifying preferred target

sequences, and for engineering zinc finger proteins to bind to such preferred target sequences, are disclosed in co-owned WO 00/42219.

A designed zinc finger protein is a protein not occurring in nature whose design/composition results principally from rational criteria. Rational criteria for design
5 include application of substitution rules and computerized algorithms for processing information in a database storing information of existing ZFP designs and binding data.

A selected zinc finger protein is a protein not found in nature whose production results primarily from an empirical process such as phage display.

The term naturally-occurring is used to describe an object that can be found in
10 nature as distinct from being artificially produced by man. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally-occurring. Generally, the term naturally-occurring refers to an object as present in a non-pathological (undiseased) individual, such as would be typical
15 for the species.

A nucleic acid is operably linked when it is placed into a functional relationship with another nucleic acid sequence. For instance, a promoter or enhancer is operably linked to a coding sequence if it increases the transcription of the coding sequence. Operably linked means that the DNA sequences being linked are typically contiguous
20 and, where necessary to join two protein coding regions, contiguous and in reading frame. However, since enhancers generally function when separated from the promoter by up to several kilobases or more and intronic sequences may be of variable lengths, some polynucleotide elements may be operably linked but not contiguous.

A specific binding affinity between, for example, a ZFP and a specific target site
25 means a binding affinity of at least $1 \times 10^6 \text{ M}^{-1}$.

The terms "modulating expression" "inhibiting expression" and "activating expression" of a gene refer to the ability of a zinc finger protein to activate or inhibit transcription of a gene. Activation includes prevention of subsequent transcriptional inhibition (i.e., prevention of repression of gene expression) and inhibition includes
30 prevention of subsequent transcriptional activation (i.e., prevention of gene activation). Modulation can be assayed by determining any parameter that is indirectly or directly

affected by the expression of the target gene. Such parameters include, e.g., changes in RNA or protein levels, changes in protein activity, changes in product levels, changes in downstream gene expression, changes in reporter gene transcription (luciferase, CAT, beta-galactosidase, GFP (see, e.g., Mistili & Spector, *Nature Biotechnology* 15:961-964 (1997))); changes in signal transduction, phosphorylation and dephosphorylation, receptor-ligand interactions, second messenger concentrations (e.g., cGMP, cAMP, IP3, and Ca²⁺), cell growth, neovascularization, *in vitro*, *in vivo*, and *ex vivo*. Such functional effects can be measured by any means known to those skilled in the art, e.g., measurement of RNA or protein levels, measurement of RNA stability, identification of downstream or reporter gene expression, e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, ligand binding assays; changes in intracellular second messengers such as cGMP and inositol triphosphate (IP3); changes in intracellular calcium levels; cytokine release, and the like.

A "regulatory domain" refers to a protein or a protein subsequence that has transcriptional modulation activity. Typically, a regulatory domain is covalently or non-covalently linked to a ZFP to modulate transcription. Alternatively, a ZFP can act alone, without a regulatory domain, or with multiple regulatory domains to modulate transcription.

A D-able subsite within a target site has the motif 5'NNGK3'. A target site containing one or more such motifs is sometimes described as a D-able target site. A zinc finger appropriately designed to bind to a D-able subsite is sometimes referred to as a D-able finger. Likewise a zinc finger protein containing at least one finger designed or selected to bind to a target site including at least one D-able subsite is sometimes referred to as a D-able zinc finger protein.

DETAILED DESCRIPTION

I. General

Tables 1-5 list a collection of nonnaturally occurring zinc finger protein sequences and their corresponding target sites. The first column of each table is an internal reference number. The second column lists a 9 or 10 base target site bound by a three-finger zinc finger protein, with the target sites listed in 5' to 3' orientation. The

third column provides SEQ ID NOs for the target site sequences listed in column 2. The fourth, sixth and eighth columns list amino acid residues from the first, second and third fingers, respectively, of a zinc finger protein which recognizes the target sequence listed in the second column. For each finger, seven amino acids, occupying positions -1 to +6 of the finger, are listed. The numbering convention for zinc fingers is defined below. Columns 5, 7 and 9 provide SEQ ID NOs for the amino acid sequences listed in columns 4, 6 and 8, respectively. The final column of each table lists the binding affinity (*i.e.*, the K_d in nM) of the zinc finger protein for its target site. Binding affinities are measured as described below.

Each finger binds to a triplet of bases within a corresponding target sequence. The first finger binds to the first triplet starting from the 3' end of a target site, the second finger binds to the second triplet, and the third finger binds the third (*i.e.*, the 5'-most) triplet of the target sequence. For example, the RSDSLTS finger (SEQ ID NO: 646) of SBS# 201 (Table 2) binds to 5'TTG3', the ERSTLTR finger (SEQ ID NO: 851) binds to 5'GCC3' and the QRADLRR finger (SEQ ID NO: 1056) binds to 5'GCA3'.

Table 6 lists a collection of consensus sequences for zinc fingers and the target sites bound by such sequences. Conventional one letter amino acid codes are used to designate amino acids occupying consensus positions. The symbol "X" designates a nonconsensus position that can in principle be occupied by any amino acid. In most zinc fingers of the C_2H_2 type, binding specificity is principally conferred by residues -1, +2, +3 and +6. Accordingly, consensus sequence determining binding specificity typically include at least these residues. Consensus sequences are useful for designing zinc fingers to bind to a given target sequence. Residues occupying other positions can be selected based on sequences in Tables 1-5, or other known zinc finger sequences. Alternatively, these positions can be randomized with a plurality of candidate amino acids and screened against one or more target sequences to refine binding specificity or improve binding specificity. In general, the same consensus sequence can be used for design of a zinc finger regardless of the relative position of that finger in a multi-finger zinc finger protein. For example, the sequence RXDNXXR can be used to design a N-terminal, central or C-terminal finger of three finger protein. However, some consensus sequences are most suitable for designing a zinc finger to occupy a particular position in a multi-

finger protein. For example, the consensus sequence RXDHXXQ is most suitable for designing a C-terminal finger of a three-finger protein.

II. Characteristics of Zinc Finger Proteins

5 Zinc finger proteins are formed from zinc finger components. For example, zinc finger proteins can have one to thirty-seven fingers, commonly having 2, 3, 4, 5 or 6 fingers. A zinc finger protein recognizes and binds to a target site (sometimes referred to as a target segment) that represents a relatively small subsequence within a target gene.

Each component finger of a zinc finger protein can bind to a subsite within the target site.

10 The subsite includes a triplet of three contiguous bases all on the same strand (sometimes referred to as the target strand). The subsite may or may not also include a fourth base on the opposite strand that is the complement of the base immediately 3' of the three contiguous bases on the target strand. In many zinc finger proteins, a zinc finger binds to its triplet subsite substantially independently of other fingers in the same zinc finger protein. Accordingly, the binding specificity of zinc finger protein containing multiple
15 fingers is usually approximately the aggregate of the specificities of its component fingers. For example, if a zinc finger protein is formed from first, second and third fingers that individually bind to triplets XXX, YYY, and ZZZ, the binding specificity of the zinc finger protein is 3'XXX YYY ZZZ5'.

20 The relative order of fingers in a zinc finger protein from N-terminal to C-terminal determines the relative order of triplets in the 3' to 5' direction in the target.

For example, if a zinc finger protein comprises from N-terminal to C-terminal first, second and third fingers that individually bind, respectively, to triplets 5' GAC3', 5'GTA3' and 5'GGC3' then the zinc finger protein binds to the target segment

25 3'CAGATGCGG5'. If the zinc finger protein comprises the fingers in another order, for example, second finger, first finger, third finger, then the zinc finger protein binds to a target segment comprising a different permutation of triplets, in this example, 3'ATGCAGCGG5' (see Berg & Shi, *Science* 271, 1081-1086 (1996)). The assessment of binding properties of a zinc finger protein as the aggregate of its component fingers
30 may, in some cases, be influenced by context-dependent interactions of multiple fingers binding in the same protein.

Two or more zinc finger proteins can be linked to have a target specificity that is the aggregate of that of the component zinc finger proteins (see e.g., Kim & Pabo, *PNAS* 95, 2812-2817 (1998)). For example, a first zinc finger protein having first, second and third component fingers that respectively bind to XXX, YYY and ZZZ can be linked to a second zinc finger protein having first, second and third component fingers with binding specificities, AAA, BBB and CCC. The binding specificity of the combined first and second proteins is thus 3'XXXYYYZZZ___AAABBBCCC5', where the underline indicates a short intervening region (typically 0-5 bases of any type). In this situation, the target site can be viewed as comprising two target segments separated by an intervening segment.

Linkage can be accomplished using any of the following peptide linkers.
T G E K P: (SEQ. ID. No:2) (Liu et al., 1997, supra.); (G4S)_n (SEQ. ID. No:3) (Kim et al., *PNAS* 93, 1156-1160 (1996.); GGRRGGGS; (SEQ. ID. No:4) LRQRDGERP; (SEQ. ID. No:5) LRQKDGGGSERP; (SEQ. ID. No:6) LRQKD(G3S)₂ ERP (SEQ. ID. No:7)
Alternatively, flexible linkers can be rationally designed using computer programs capable of modeling both DNA-binding sites and the peptides themselves or by phage display methods. In a further variation, noncovalent linkage can be achieved by fusing two zinc finger proteins with domains promoting heterodimer formation of the two zinc finger proteins. For example, one zinc finger protein can be fused with fos and the other with jun (see Barbas et al., WO 95/119431).

Linkage of two zinc finger proteins is advantageous for conferring a unique binding specificity within a mammalian genome. A typical mammalian diploid genome consists of 3×10^9 bp. Assuming that the four nucleotides A, C, G, and T are randomly distributed, a given 9 bp sequence is present ~23,000 times. Thus a ZFP recognizing a 9 bp target with absolute specificity would have the potential to bind to ~23,000 sites within the genome. An 18 bp sequence is present once in 3.4×10^{10} bp, or about once in a random DNA sequence whose complexity is ten times that of a mammalian genome.

A component finger of zinc finger protein typically contains about 30 amino acids and has the following motif (N-C) :

(SEQ. ID. No:8)
Cys- (X)₂₋₄-Cys-X.X.X.X.X.X.X.X.X.X.X.X-**His**-(X)₃₋₅-His

-1 1 2 3 4 5 6 7

The two invariant histidine residues and two invariant cysteine residues in a single beta turn are co-ordinated through zinc (see, e.g., Berg & Shi, *Science* 271, 1081-1085 (1996)). The above motif shows a numbering convention that is standard in the field for the region of a zinc finger conferring binding specificity. The amino acid on the left (N-terminal side) of the first invariant His residues is assigned the number +6, and other amino acids further to the left are assigned successively decreasing numbers. The alpha helix begins at residue 1 and extends to the residue following the second conserved histidine. The entire helix is therefore of variable length, between 11 and 13 residues.

The process of designing or selecting a nonnaturally occurring or variant ZFP typically starts with a natural ZFP as a source of framework residues. The process of design or selection serves to define nonconserved positions (i.e., positions -1 to +6) so as to confer a desired binding specificity. One suitable ZFP is the DNA binding domain of the mouse transcription factor Zif268. The DNA binding domain of this protein has the amino acid sequence:

YACPVESCDRRFSRSDDELTRHIRIHTGQKP (F1) (SEQ. ID No:9)
FQCRICMRNFSRSDHLTTHIRHTGQKP (F2) (SEQ. ID. No:10)
FACDICGRKFARSDEKRRHTKIHRLRQK (F3) SEQ. ID. No:11)
and binds to a target 5' GCG TGG GCG 3' (SEQ ID No:12).

Another suitable natural zinc finger protein as a source of framework residues is Sp-1. The Sp-1 sequence used for construction of zinc finger proteins corresponds to amino acids 531 to 624 in the Sp-1 transcription factor. This sequence is 94 amino acids in length. The amino acid sequence of Sp-1 is as follows:

PGKKKQHICHIQGCGKVYGKTSHLRAHLRWHTGERP
FMCTWSYCGKRFRSDDELQRHKRTHHTGEEKK
FACPECPKRFMRSDHLSKHIKTHQNKKG (SEQ. ID. No:13)
Sp-1 binds to a target site 5'GGG GCG GGG3' (SEQ ID No: 14).

An alternate form of Sp-1, an Sp-1 consensus sequence, has the following amino acid sequence:

meklrngsgd
PGKKKQHACPECGKSFSKSSHLRAHQRTHTGERP

YKCPECGKSFSRSDELQRHQRTHTGEKP

YKCPECGKSFSRSDHLSKHQORTHQNKKG (SEQ. ID. No:15) (lower case letters are a leader sequence from Shi & Berg, *Chemistry and Biology* 1, 83-89. (1995). The optimal binding sequence for the Sp-1 consensus sequence is 5'GGGGCGGGG3' (SEQ ID No:

5 16) . Other suitable ZFPs are described below.

There are a number of substitution rules that assist rational design of some zinc finger proteins (see Desjarlais & Berg, *PNAS* 90, 2256-2260 (1993); Choo & Klug, *PNAS* 91, 11163-11167 (1994); Desjarlais & Berg, *PNAS* 89, 7345-7349 (1992); Jamieson et al., supra; Choo et al., WO 98/53057, WO 98/53058; WO 98/53059; WO 98/53060).

10 Many of these rules are supported by site-directed mutagenesis of the three-finger domain of the ubiquitous transcription factor, Sp-1 (Desjarlais and Berg, 1992; 1993). One of these rules is that a 5' G in a DNA triplet can be bound by a zinc finger incorporating arginine at position 6 of the recognition helix. Another substitution rule is that a G in the middle of a subsite can be recognized by including a histidine residue at position 3 of a
15 zinc finger. A further substitution rule is that asparagine can be incorporated to recognize A in the middle of triplet, aspartic acid, glutamic acid, serine or threonine can be incorporated to recognize C in the middle of triplet, and amino acids with small side chains such as alanine can be incorporated to recognize T in the middle of triplet. A further substitution rule is that the 3' base of triplet subsite can be recognized by
20 incorporating the following amino acids at position -1 of the recognition helix: arginine to recognize G, glutamine to recognize A, glutamic acid (or aspartic acid) to recognize C, and threonine to recognize T. Although these substitution rules are useful in designing zinc finger proteins they do not take into account all possible target sites. Furthermore, the assumption underlying the rules, namely that a particular amino acid in a zinc finger
25 is responsible for binding to a particular base in a subsite is only approximate. Context-dependent interactions between proximate amino acids in a finger or binding of multiple amino acids to a single base or vice versa can cause variation of the binding specificities predicted by the existing substitution rules.

30 The technique of phage display provides a largely empirical means of generating zinc finger proteins with a desired target specificity (see e.g., Rebar, US 5,789,538; Choo et al., WO 96/06166; Barbas et al., WO 95/19431 and WO 98/543111; Jamieson et al.,

supra). The method can be used in conjunction with, or as an alternative to rational design. The method involves the generation of diverse libraries of mutagenized zinc finger proteins, followed by the isolation of proteins with desired DNA-binding properties using affinity selection methods. To use this method, the experimenter typically proceeds as follows. First, a gene for a zinc finger protein is mutagenized to introduce diversity into regions important for binding specificity and/or affinity. In a typical application, this is accomplished via randomization of a single finger at positions -1, +2, +3, and +6, and sometimes accessory positions such as +1, +5, +8 and +10. Next, the mutagenized gene is cloned into a phage or phagemid vector as a fusion with gene III of a filamentous phage, which encodes the coat protein pIII. The zinc finger gene is inserted between segments of gene III encoding the membrane export signal peptide and the remainder of pIII, so that the zinc finger protein is expressed as an amino-terminal fusion with pIII or in the mature, processed protein. When using phagemid vectors, the mutagenized zinc finger gene may also be fused to a truncated version of gene III encoding, minimally, the C-terminal region required for assembly of pIII into the phage particle. The resultant vector library is transformed into *E. coli* and used to produce filamentous phage which express variant zinc finger proteins on their surface as fusions with the coat protein pIII. If a phagemid vector is used, then this step requires superinfection with helper phage. The phage library is then incubated with target DNA site, and affinity selection methods are used to isolate phage which bind target with high affinity from bulk phage. Typically, the DNA target is immobilized on a solid support, which is then washed under conditions sufficient to remove all but the tightest binding phage. After washing, any phage remaining on the support are recovered via elution under conditions which disrupt zinc finger – DNA binding. Recovered phage are used to infect fresh *E. coli*., which is then amplified and used to produce a new batch of phage particles. Selection and amplification are then repeated as many times as is necessary to enrich the phage pool for tight binders such that these may be identified using sequencing and/or screening methods. Although the method is illustrated for pIII fusions, analogous principles can be used to screen ZFP variants as pVIII fusions.

In certain embodiments, the sequence bound by a particular zinc finger protein is determined by conducting binding reactions (see, *e.g.*, conditions for determination of K_d ,

infra) between the protein and a pool of randomized double-stranded oligonucleotide sequences. The binding reaction is analyzed by an electrophoretic mobility shift assay (EMSA), in which protein-DNA complexes undergo retarded migration in a gel and can be separated from unbound nucleic acid. Oligonucleotides which have bound the finger
 5 are purified from the gel and amplified, for example, by a polymerase chain reaction. The selection (*i.e.* binding reaction and EMSA analysis) is then repeated as many times as desired, with the selected oligonucleotide sequences. In this way, the binding specificity of a zinc finger protein having a particular amino acid sequence is determined.

Zinc finger proteins are often expressed with a heterologous domain as fusion
 10 proteins. Common domains for addition to the ZFP include, e.g., transcription factor domains (activators, repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers
 15 (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., methyltransferases, topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for repressing expression of a target gene is a KRAB repression domain from the human KOX-1 protein (Thiesen et al.,
 20 *New Biologist* 2, 363-374 (1990); Margolin et al., *Proc. Natl. Acad. Sci. USA* 91, 4509-4513 (1994); Pengue et al., *Nucl. Acids Res.* 22:2908-2914 (1994); Witzgall et al., *Proc. Natl. Acad. Sci. USA* 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., *J. Virol.* 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., *Curr. Opin. Cell. Biol.*
 25 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, *J. Virol.* 72:5610-5618 (1998) and Doyle & Hunt, *Neuroreport* 8:2937-2942 (1997)); Liu et al., *Cancer Gene Ther.* 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., *EMBO J.* 11, 4961-4968 (1992)).

An important factor in the administration of polypeptide compounds, such as the
 30 ZFPs, is ensuring that the polypeptide has the ability to traverse the plasma membrane of a cell, or the membrane of an intra-cellular compartment such as the nucleus. Cellular

membranes are composed of lipid-protein bilayers that are freely permeable to small, nonionic lipophilic compounds and are inherently impermeable to polar compounds, macromolecules, and therapeutic or diagnostic agents. However, proteins and other compounds such as liposomes have been described, which have the ability to translocate polypeptides such as ZFPs across a cell membrane.

For example, “membrane translocation polypeptides” have amphiphilic or hydrophobic amino acid subsequences that have the ability to act as membrane-translocating carriers. In one embodiment, homeodomain proteins have the ability to translocate across cell membranes. The shortest internalizable peptide of a homeodomain protein, Antennapedia, was found to be the third helix of the protein, from amino acid position 43 to 58 (*see, e.g., Prochiantz, Current Opinion in Neurobiology* 6:629-634 (1996)). Another subsequence, the h (hydrophobic) domain of signal peptides, was found to have similar cell membrane translocation characteristics (*see, e.g., Lin et al., J. Biol. Chem.* 270:1 4255-14258 (1995)).

Examples of peptide sequences which can be linked to a ZFP, for facilitating uptake of ZFP into cells, include, but are not limited to: an 11 amino acid peptide of the tat protein of HIV; a 20 residue peptide sequence which corresponds to amino acids 84-103 of the p16 protein (*see Fahraeus et al., Current Biology* 6:84 (1996)); the third helix of the 60-amino acid long homeodomain of Antennapedia (Derossi *et al., J. Biol. Chem.* 269:10444 (1994)); the h region of a signal peptide such as the Kaposi fibroblast growth factor (K-FGF) h region (Lin *et al., supra*); or the VP22 translocation domain from HSV (Elliot & O’Hare, *Cell* 88:223-233 (1997)). Other suitable chemical moieties that provide enhanced cellular uptake may also be chemically linked to ZFPs.

Toxin molecules also have the ability to transport polypeptides across cell membranes. Often, such molecules are composed of at least two parts (called “binary toxins”): a translocation or binding domain or polypeptide and a separate toxin domain or polypeptide. Typically, the translocation domain or polypeptide binds to a cellular receptor, and then the toxin is transported into the cell. Several bacterial toxins, including *Clostridium perfringens* iota toxin, diphtheria toxin (DT), *Pseudomonas* exotoxin A (PE), pertussis toxin (PT), *Bacillus anthracis* toxin, and pertussis adenylate cyclase (CYA), have been used in attempts to deliver peptides to the cell cytosol as

internal or amino-terminal fusions (Arora *et al.*, *J. Biol. Chem.*, 268:3334-3341 (1993); Perelle *et al.*, *Infect. Immun.*, 61:5147-5156 (1993); Stenmark *et al.*, *J. Cell Biol.* 113:1025-1032 (1991); Donnelly *et al.*, *PNAS* 90:3530-3534 (1993); Carbonetti *et al.*, *Abstr. Annu. Meet. Am. Soc. Microbiol.* 95:295 (1995); Sebo *et al.*, *Infect. Immun.* 63:3851-3857 (1995); Klimpel *et al.*, *PNAS U.S.A.* 89:10277-10281 (1992); and Novak *et al.*, *J. Biol. Chem.* 267:17186-17193 (1992)).

Such subsequences can be used to translocate ZFPs across a cell membrane. ZFPs can be conveniently fused to or derivatized with such sequences. Typically, the translocation sequence is provided as part of a fusion protein. Optionally, a linker can be used to link the ZFP and the translocation sequence. Any suitable linker can be used, e.g., a peptide linker.

III. Position Dependence Of Subsite Recognition By Zinc Fingers

A number of the polypeptides disclosed herein have been characterized using the methods disclosed in parent application Serial No. 09/716,637 (the disclosure of which is hereby incorporated by reference in its entirety); in particular with respect to the effect of their position, within a multi-finger protein, on their sequence specificity. The results of these investigations provide a set of zinc finger sequences that are optimized for recognition of certain triplet target subsites whose 5'-most nucleotide is a G (*i.e.*, GNN triplet subsites). Thus, particular zinc finger sequences which recognize each of the GNN triplet subsites, from each position of a three-finger zinc finger protein, are provided. See Figure 2. It will be clear to those of skill in the art that the optimized, position-specific zinc finger sequences disclosed herein for recognition of GNN target subsites are not limited to use in three-finger proteins. For example, they are also useful in six-finger proteins, which can be made by linkage of two three-finger proteins.

A number of zinc finger amino acid sequences which are reported to bind to target subsites in which the 5'-most nucleotide residue is G (*i.e.*, GNN subsites) have recently been disclosed. Segal *et al.* (1999) *Proc. Natl. Acad. Sci. USA* 96:2758-2763; Drier *et al.* (2000) *J. Mol. Biol.* 303:489-502; U.S. Patent No. 6,140,081. These GNN-binding zinc fingers were obtained by selection of finger 2 sequences from phage display libraries of three-finger proteins, in which certain amino acid residues of finger 2 had been

randomized. Due to the manner in which they were selected, it is not clear whether these sequences would have the same target subsite specificity if they were present in the F1 and/or F3 positions.

Use of the methods and compositions disclosed herein has now allowed
5 identification of specific zinc finger sequences that bind each of the 16 GNN triplet subsites, and for the first time, provides zinc finger sequences that are optimized for recognition of these triplet subsites in a position-dependent fashion. Moreover, *in vivo* studies of these optimized designs reveal that the functionality of a ZFP is correlated with its binding affinity to its target sequence. See Example 6, *infra*.

10 As a result of the discovery, disclosed herein, that sequence recognition by zinc fingers is position-dependent, it is clear that existing design rules will not, in and of themselves, be applicable to every situation in which it is necessary to construct a sequence-specific ZFP. The results disclosed herein show that many zinc fingers that are constructed based on design rules exhibit the sequence specificity predicted by those
15 design rules only at certain finger positions. The position-specific zinc fingers disclosed herein are likely to function more efficiently *in vivo* and in cultured cells, with fewer nonspecific effects. Highly specific ZFPs, made using position-specific zinc fingers, will be useful tools in studying gene function and will find broad applications in areas as diverse as human therapeutics and plant engineering.

20 **IV. Production of Zinc Finger Proteins**

ZFP polypeptides and nucleic acids encoding the same can be made using routine techniques in the field of recombinant genetics. Basic texts disclosing the general methods include Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd ed.
25 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel et al., eds., 1994)). In addition, nucleic acids less than about 100 bases can be custom ordered from any of a variety of commercial sources, such as The Midland Certified Reagent Company (mcrc@oligos.com), The Great American Gene Company (<http://www.genco.com>),
30 ExpressGen Inc. (www.expressgen.com), Operon Technologies Inc. (Alameda, CA). Similarly, peptides can be custom ordered from any of a variety of sources, such as

PeptidoGenic (pkim@ccnet.com), HTI Bio-products, inc. (<http://www.htibio.com>), BMA Biomedicals Ltd (U.K.), Bio.Synthesis, Inc.

Oligonucleotides can be chemically synthesized according to the solid phase phosphoramidite triester method first described by Beaucage & Caruthers, *Tetrahedron Letts.* 22:1859-1862 (1981), using an automated synthesizer, as described in Van Devanter et al., *Nucleic Acids Res.* 12:6159-6168 (1984). Purification of oligonucleotides is by either denaturing polyacrylamide gel electrophoresis or by reverse phase HPLC. The sequence of the cloned genes and synthetic oligonucleotides can be verified after cloning using, e.g., the chain termination method for sequencing double-stranded templates of Wallace et al., *Gene* 16:21-26 (1981).

Two alternative methods are typically used to create the coding sequences required to express newly designed DNA-binding peptides. One protocol is a PCR-based assembly procedure that utilizes six overlapping oligonucleotides (Fig. 1). Three oligonucleotides (oligos 1, 3, and 5 in Figure 1) correspond to “universal” sequences that encode portions of the DNA-binding domain between the recognition helices. These oligonucleotides typically remain constant for all zinc finger constructs. The other three “specific” oligonucleotides (oligos 2, 4, and 6 in Fig. 1) are designed to encode the recognition helices. These oligonucleotides contain substitutions primarily at positions - 1, 2, 3 and 6 on the recognition helices making them specific for each of the different DNA-binding domains.

The PCR synthesis is carried out in two steps. First, a double stranded DNA template is created by combining the six oligonucleotides (three universal, three specific) in a four cycle PCR reaction with a low temperature annealing step, thereby annealing the oligonucleotides to form a DNA “scaffold.” The gaps in the scaffold are filled in by high-fidelity thermostable polymerase, the combination of Taq and Pfu polymerases also suffices. In the second phase of construction, the zinc finger template is amplified by external primers designed to incorporate restriction sites at either end for cloning into a shuttle vector or directly into an expression vector.

An alternative method of cloning the newly designed DNA-binding proteins relies on annealing complementary oligonucleotides encoding the specific regions of the desired ZFP. This particular application requires that the oligonucleotides be

phosphorylated prior to the final ligation step. This is usually performed before setting up the annealing reactions. In brief, the “universal” oligonucleotides encoding the constant regions of the proteins (oligos 1, 2 and 3 of above) are annealed with their complementary oligonucleotides. Additionally, the “specific” oligonucleotides encoding the finger recognition helices are annealed with their respective complementary oligonucleotides. These complementary oligos are designed to fill in the region which was previously filled in by polymerase in the above-mentioned protocol. The complementary oligos to the common oligos 1 and finger 3 are engineered to leave overhanging sequences specific for the restriction sites used in cloning into the vector of choice in the following step. The second assembly protocol differs from the initial protocol in the following aspects: the “scaffold” encoding the newly designed ZFP is composed entirely of synthetic DNA thereby eliminating the polymerase fill-in step, additionally the fragment to be cloned into the vector does not require amplification. Lastly, the design of leaving sequence-specific overhangs eliminates the need for restriction enzyme digests of the inserting fragment. Alternatively, changes to ZFP recognition helices can be created using conventional site-directed mutagenesis methods.

Both assembly methods require that the resulting fragment encoding the newly designed ZFP be ligated into a vector. Ultimately, the ZFP-encoding sequence is cloned into an expression vector. Expression vectors that are commonly utilized include, but are not limited to, a modified pMAL-c2 bacterial expression vector (New England BioLabs or an eukaryotic expression vector, pcDNA (Promega). The final constructs are verified by sequence analysis.

Any suitable method of protein purification known to those of skill in the art can be used to purify ZFPs (see, Ausubel, supra, Sambrook, supra). In addition, any suitable host can be used for expression, e.g., bacterial cells, insect cells, yeast cells, mammalian cells, and the like.

Expression of a zinc finger protein fused to a maltose binding protein (MBP-ZFP) in bacterial strain JM109 allows for straightforward purification through an amylose column (NEB). High expression levels of the zinc finger chimeric protein can be obtained by induction with IPTG since the MBP-ZFP fusion in the pMal-c2 expression plasmid is under the control of the tac promoter (NEB). Bacteria containing the MBP-

ZFP fusion plasmids are inoculated into 2xYT medium containing 10 μ M ZnCl₂, 0.02% glucose, plus 50 μ g/ml ampicillin and shaken at 37°C. At mid-exponential growth IPTG is added to 0.3 mM and the cultures are allowed to shake. After 3 hours the bacteria are harvested by centrifugation, disrupted by sonication or by passage through a french pressure cell or through the use of lysozyme, and insoluble material is removed by centrifugation. The MBP-ZFP proteins are captured on an amylose-bound resin, washed extensively with buffer containing 20 mM Tris-HCl (pH 7.5), 200 mM NaCl, 5 mM DTT and 50 μ M ZnCl₂, then eluted with maltose in essentially the same buffer (purification is based on a standard protocol from NEB). Purified proteins are quantitated and stored for biochemical analysis.

The dissociation constants of the purified proteins, e.g., K_d, are typically characterized via electrophoretic mobility shift assays (EMSA) (Buratowski & Chodosh, in *Current Protocols in Molecular Biology* pp. 12.2.1-12.2.7 (Ausubel ed., 1996)). Affinity is measured by titrating purified protein against a fixed amount of labeled double-stranded oligonucleotide target. The target typically comprises the natural binding site sequence flanked by the 3 bp found in the natural sequence and additional, constant flanking sequences. The natural binding site is typically 9 bp for a three-finger protein and 2 x 9 bp + intervening bases for a six finger ZFP. The annealed oligonucleotide targets possess a 1 base 5' overhang which allows for efficient labeling of the target with T4 phage polynucleotide kinase. For the assay the target is added at a concentration of 1 nM or lower (the actual concentration is kept at least 10-fold lower than the expected dissociation constant), purified ZFPs are added at various concentrations, and the reaction is allowed to equilibrate for at least 45 min. In addition the reaction mixture also contains 10 mM Tris (pH 7.5), 100 mM KCl, 1 mM MgCl₂, 0.1 mM ZnCl₂, 5 mM DTT, 10% glycerol, 0.02% BSA. (NB: in earlier assays poly d(IC) was also added at 10-100 μ g/ μ l.)

The equilibrated reactions are loaded onto a 10% polyacrylamide gel, which has been pre-run for 45 min in Tris/glycine buffer, then bound and unbound labeled target is resolved by electrophoresis at 150V. (alternatively, 10-20% gradient Tris-HCl gels, containing a 4% polyacrylamide stacker, can be used) The dried gels are visualized by

autoradiography or phosphorimaging and the apparent K_d is determined by calculating the protein concentration that gives half-maximal binding.

The assays can also include determining active fractions in the protein preparations. Active fractions are determined by stoichiometric gel shifts where proteins are titrated against a high concentration of target DNA. Titrations are done at 100, 50, and 25% of target (usually at micromolar levels).

V. Applications of Engineered Zinc Finger Proteins

ZFPs that bind to a particular target gene, and the nucleic acids encoding them, can be used for a variety of applications. These applications include therapeutic methods in which a ZFP or a nucleic acid encoding it is administered to a subject and used to modulate the expression of a target gene within the subject. *See*, for example, co-owned WO 00/41566. The modulation can be in the form of repression, for example, when the target gene resides in a pathological infecting microorganisms, or in an endogenous gene of the patient, such as an oncogene or viral receptor, that is contributing to a disease state. Alternatively, the modulation can be in the form of activation when activation of expression or increased expression of an endogenous cellular gene can ameliorate a diseased state. For such applications, ZFPs, or more typically, nucleic acids encoding them are formulated with a pharmaceutically acceptable carrier as a pharmaceutical composition.

Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed. 1985)). The ZFPs, alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like. Formulations suitable for parenteral administration, such as, for example, by intravenous, intramuscular, intradermal, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and

non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. Compositions can be administered, for example, by intravenous infusion, orally, topically, intraperitoneally, intravesically or intrathecally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Injection solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described.

The dose administered to a patient should be sufficient to effect a beneficial therapeutic response in the patient over time. The dose is determined by the efficacy and K_d of the particular ZFP employed, the target cell, and the condition of the patient, as well as the body weight or surface area of the patient to be treated. The size of the dose also is determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular compound or vector in a particular patient

In other applications, ZFPs are used in diagnostic methods for sequence specific detection of target nucleic acid in a sample. For example, ZFPs can be used to detect variant alleles associated with a disease or phenotype in patient samples. As an example, ZFPs can be used to detect the presence of particular mRNA species or cDNA in a complex mixtures of mRNAs or cDNAs. As a further example, ZFPs can be used to quantify copy number of a gene in a sample. For example, detection of loss of one copy of a p53 gene in a clinical sample is an indicator of susceptibility to cancer. In a further example, ZFPs are used to detect the presence of pathological microorganisms in clinical samples. This is achieved by using one or more ZFPs specific to genes within the microorganism to be detected. A suitable format for performing diagnostic assays employs ZFPs linked to a domain that allows immobilization of the ZFP on an ELISA plate. The immobilized ZFP is contacted with a sample suspected of containing a target nucleic acid under conditions in which binding can occur. Typically, nucleic acids in the sample are labeled (e.g., in the course of PCR amplification). Alternatively, unlabelled probes can be detected using a second labelled probe. After washing, bound-labelled nucleic acids are detected.

ZFPs also can be used for assays to determine the phenotype and function of gene expression. Current methodologies for determination of gene function rely primarily

upon either overexpression or removing (knocking out completely) the gene of interest from its natural biological setting and observing the effects. The phenotypic effects observed indicate the role of the gene in the biological system.

One advantage of ZFP-mediated regulation of a gene relative to conventional knockout analysis is that expression of the ZFP can be placed under small molecule control. By controlling expression levels of the ZFPs, one can in turn control the expression levels of a gene regulated by the ZFP to determine what degree of repression or stimulation of expression is required to achieve a given phenotypic or biochemical effect. This approach has particular value for drug development. By putting the ZFP under small molecule control, problems of embryonic lethality and developmental compensation can be avoided by switching on the ZFP repressor at a later stage in mouse development and observing the effects in the adult animal. Transgenic mice having target genes regulated by a ZFP can be produced by integration of the nucleic acid encoding the ZFP at any site *in trans* to the target gene. Accordingly, homologous recombination is not required for integration of the nucleic acid. Further, because the ZFP is trans-dominant, only one chromosomal copy is needed and therefore functional knock-out animals can be produced without backcrossing.

All references cited above are hereby incorporated by reference in their entirety for all purposes.

EXAMPLES

Example 1: Initial design of zinc finger proteins and determination of binding affinity

Initial ZFP designs were based on existing design rules, correspondence regimes and ZFP directories, including those disclosed herein (*see* Tables 1-5) and also in WO 98/53058; WO 98/530059; WO 98/53060 and co-owned US patent application Serial No. 09/444,241. *See* also WO 00/42219. Amino acid sequences were conceptually designed using amino acids 532-624 of the human transcription factor Sp1 as a backbone. Polynucleotides encoding designed ZFPs were assembled using a Polymerase Chain Reaction (PCR)-based procedure that utilizes six overlapping oligonucleotides. PCR products were directly cloned cloning into the Tac promoter

vector, pMal-c2 (New England Biolabs, Beverly, MA) using the KpnI and BamHI restriction sites. The encoded maltose binding protein-ZFP fusion polypeptides were purified according to the manufacturer's procedures (New England Biolabs, Beverly, MA). Binding affinity was measured by gel mobility-shift analysis. All of these procedures are described in detail in co-owned WO 00/41566 and WO 00/42219, as well as in Zhang *et al.* (2000) *J. Biol. Chem.* **275**:33,850-33,860 and Liu *et al.* (2001) *J. Biol. Chem.* **276**:11,323-11,334; the disclosures of which are hereby incorporated by reference in their entireties.

Example 2: Optimization of binding specificity by site selection

Designed ZFPs were tested for binding specificity using site selection methods disclosed in parent application USSN 09/716,637. Briefly, designed proteins were incubated with a population of labeled, double-stranded oligonucleotides comprising a library of all possible 9- or 10-nucleotide target sequences. Five nanomoles of labeled oligonucleotides were incubated with protein, at a protein concentration 4-fold above its K_d for its target sequence. The mixture was subjected to gel electrophoresis, and bound oligonucleotides were identified by mobility shift, and extracted from the gel. The purified bound oligonucleotides were amplified, and the amplification products were used for a subsequent round of selection. At each round of selection, the protein concentration was decreased by 2 fold. After 3-5 rounds of selection, amplification products were cloned into the TOPO TA cloning vector (Invitrogen, Carlsbad, CA), and the nucleotide sequences of approximately 20 clones were determined. The identities of the target sites bound by a designed protein were determined from the sequences and expressed as a compilation of subsite binding sequences.

Example 3: Comparison of site selection results with binding affinity

To test the correlation between site selection results and the affinity of binding of a ZFP to various related targets, site selection experiments were conducted on 2 three-finger ZFPs, denoted ZFP1 and ZFP2, and the site selection results were compared with K_d measurements obtained from quantitative gel-mobility shift assays using the same ZFPs and target sites. Each ZFP was constructed, based on design rules, to bind to a

particular nine-nucleotide target sequence (comprising 3 three-nucleotide subsites), as shown in Figure 1. Site selection results and affinity measurements are also shown in Figure 1. The site selection results showed that fingers 1 and 3 of both the ZFP1 and ZFP2 proteins preferentially selected their intended target sequences. However, the
5 second finger of each ZFP preferentially selected subsites other than those to which they were designed to bind (*e.g.*, F2 of ZFP1 was designed to bind TCG, but preferentially selected GTG; F2 of ZFP2 was designed to bind GGT, but preferentially selected GGA).

To confirm the site selection results, binding affinities of ZFP1 and ZFP2 were measured (see Example 1, *supra*), both to their original target sequences and to new
10 target sequences reflecting the site selection results. For example, the Mt-1 sequence contains two base changes (compared to the original target sequence for ZFP1) which result in a change in the sequence of the finger 2 subsite to GTG, reflecting the preferred finger 2 subsite sequence obtained by site selection. In agreement with the site selection results, binding of ZFP1 to the Mt-1 sequence is approximately 4-fold stronger than its
15 binding to the original target sequence (K_d of 12.5 nM compared to a K_d of 50 nM, see Figure 1).

For ZFP2, the specificity of finger 2 for the 3' base of its target subsite was tested, since, although this finger was designed to bind GGT, site selection indicated that it bound preferentially to GGA. Moreover, the site selection results predicted that finger 2
20 of ZFP2 would bind with approximately equal affinity to GGT and GGC. Accordingly, target sequences containing GGA (Mt-3) and GGC (Mt-4) at the finger 2 subsite were constructed, and binding affinities of ZFP2 to these target sequences, and to its original target sequence (containing GGT at the finger 2 subsite), were compared. In complete agreement with the site selection results, ZFP2 exhibited the strongest binding affinity for
25 the target sequence containing GGA at the finger 2 subsite (K_d of 0.5 nM, Figure 1), and its affinity for target sequences containing either GGT or GGC at the finger 2 subsite was approximately equal (K_d of 1 nM for both targets, Figure 1). Accordingly, the site selection method, in addition to being useful for iterative optimization of binding specificity, can also be used as a useful indicator of binding affinity.

Example 4: Use of site selection to identify position-dependent, GNN-binding zinc fingers

A large number of engineered ZFPs have been evaluated, by site selection, to identify zinc fingers that bind to GNN target subsites. In the course of these studies, it became apparent that the binding specificity of a particular zinc finger sequence is, in some instances, dependent upon the position of the zinc finger in the protein, and hence upon the location of the target subsite within the target sequence. For example, if one wishes to design a three-finger zinc finger protein to bind to a target sequence containing the triplet subsite GAT, it is necessary to know whether this subsite is the first, second or third subsite in the target sequence (*i.e.*, whether the GAT subsite will be bound by the first, second or third finger of the protein). Accordingly, over 110 three-finger zinc finger proteins, containing potential GNN-recognizing zinc fingers in various locations, have been evaluated by site selection experiments. Generally, several zinc finger sequences were designed to recognize each GNN triplet, and each design was tested in each of the F1, F2 and F3 positions through 4 to 6 rounds of selection.

The results of these analyses, shown in Figure 2, provide optimal position-dependent zinc finger sequences (the sequences shown represent amino acid residues –1 through +6 of the recognition helix portion of the finger) for recognition of the 16 GNN target subsites, as well as site selection results for these GNN-specific zinc fingers.

Optimal amino acid sequences for recognition of each GNN subsite from each of three positions (finger 1, finger 2 or finger 3) are thereby provided.

GNG-binding finger designs

The amino acid sequence RSDXLXR (position –1 to +6 of the recognition helix) was found to be optimal for binding to the four GNG triplets, with Asn⁺³ specifying A as the middle nucleotide; His⁺³ specifying G as the middle nucleotide; Ala⁺³ specifying T as the middle nucleotide; and Asp⁺³ specifying cytosine as the middle nucleotide. At the +5 position, Ala, Thr, Ser, and Gln, were tested, and all showed similar specificity profiles by site selection. Interestingly, and in contrast to a previous report (Swirnoff *et al.* (1995) *Mol. Cell. Biol.* **15**:2275-2287), site selection results indicated that three naturally-occurring GCG-binding fingers from zif268 and Sp1, having the amino acid sequences RSDDELTR, RSDDELQR, and RSDERKR, were not GCG-specific. Rather, each of these

fingers selected almost equal numbers of GCG and GTG sequences. Analysis of binding affinity by gel-shift experiments confirmed that finger 3 of zif268, having the sequence RSDERKR, binds GCG and GTG with approximately equal affinity.

Position dependence of GCA-, GAT-, GGT-, GAA- and GCC-binding fingers

Based on existing design rules, the amino acid sequence QSGDLTR (-1 through +6) was tested for its ability to bind the GCA triplet from three positions (F1, F2, and F3) within a three-finger ZFP. Figure 3A shows that the QSGDLTR sequence bound preferentially to the GCA triplet subsite from the F2 and F3 positions, but not from F1. In fact, the presence of QSGDLTR at the F1 position of three different three-finger ZFPs resulted predominantly in selection of GCT. Accordingly, an attempt was made to redesign this sequence to obtain specificity for GCA from the F1 position. Since the sequence $Q^{-1}G^{+2}S^{+3}R^{+6}$ had previously been selected from a randomized F1 library using GCA as target (Rebar *et al.* (1994) *Science* **263**:671-673), a D (asp) to S (ser) change was made at the +3 residue of this finger. The resulting sequence, QSGSLTR, was tested for its binding specificity by site selection and found to preferentially bind GCA, from the F1 position, in three different ZFPs (see Figure 2).

The QSGSLTR zinc finger, optimized for recognition of the GCA subsite from the F1 position, was tested for its selectivity when located at the F2 position. Accordingly, two ZFPs, one containing QSGSLTR at finger 2 and one containing QSGDLTR at finger 2 (both having identical F1 sequences and identical F3 sequences) were tested by site selection. The results indicated that, when used at the F2 position, QSGSLTR bound preferentially to GTA, rather than GCA. Thus, for optimal binding of a GCA triplet subsite from the F1 position, the amino acid sequence QSGSLTR is required; while, for optimal binding of the same subsite sequence from F2 or F3, QSGDLTR should be used. Accordingly, different zinc finger amino acid sequences may be needed to specify a particular triplet subsite sequence, depending upon the location of the subsite within the target sequence and, hence, upon the position of the finger in the protein.

Positional effects were also observed for zinc fingers recognizing GAT and GGT subsites. The zinc finger amino acid sequence QSSNLAR (-1 through +6) is expected to bind to GAT, based on design rules. However, this sequence selected GAT only from the

F1 position, and not from the F2 and F3 positions, from which the sequence GAA was preferentially bound (Figure 3B). Similarly, the amino acid sequence QSSHLTR which, based on design rules, should bind GGT, selected GGT at the F1 position, but not at the F2 and F3 positions, from which it preferentially bound GGA (Figure 3C). Conversely, the amino acid sequence TSGHLVR has previously been disclosed to recognize the triplet GGT, based on its selection from a randomized library of zif268 finger 2. U.S. Patent No. 6,140,081. However, TSGHLVR was not specific for the GGT subsite when located at the F1 position (Figure 3C). These results indicate that the binding specificity of many fingers is position dependent, and particularly point out that the sequence specificity of a zinc finger selected from a F2 library may be positionally limited.

The results shown in Figure 2 indicate that recognition of at least GAA and GCC triplets by zinc fingers is also position dependent.

These positional dependences stand in contrast to earlier published work, which suggested that zinc fingers behaved as independent modules with respect to the sequence specificity of their binding to DNA. Desjarlais *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:2256-2260.

Example 5: Characterization of EP2C

The engineered zinc finger protein EP2C binds to a target sequence, GCGGTGGCT with a dissociation constant (K_d) of 2 nM. Site selection results indicated that fingers 1 and 2 are highly specific for their target subsites, while finger 3 selects GCG (its intended target subsite) and GTG at approximately equal frequencies (Figure 4A). To confirm these observations, the binding affinities of EP2C to its cognate target sequence, and to variant target sequences, was measured by standard gel-shift analyses (see Example 1, *supra*). As standards for comparison, the binding affinities of Sp1 and zif268 to their respective targets were also measured under the same conditions, and were determined to be 40 nM for SP1 (target sequence GGGGCGGGG) and 2 nM for zif268 (target sequence GCGTGGGCG). Measurements of binding affinities confirmed that F3 of EP2C bound GTG and GCG equally well (K_d s of 2 nM), but bound GAG with a two-fold lower affinity (Figure 4B). Finger 2 was very specific for the GTG triplet, binding 15-fold less tightly to a GGG triplet (compare 2C0 and 2C3 in Figure 4B).

Finger 1 was also very specific for the GCT triplet, it bound with 4-fold lower affinity to a GAT triplet (2C4) and with 2-fold lower affinity to a GCG triplet (2C5). This example shows, once again, the high degree of correlation between site selection results and binding affinities.

5

Example 6: Evaluation of engineered ZFPs by *in vivo* functional assays

To determine whether a correlation exists between the binding affinity of a engineered ZFP to its target sequence and its functionality *in vivo*, cell-based reporter gene assays were used to analyze the functional properties of the engineered ZFP EP2C (see Example 5, *supra*). For these assays, a plasmid encoding the EP2C ZFP, fused to a VP16 transcriptional activation domain, was used to construct a stable cell line (T-Rex-293TM, Invitrogen, Carlsbad, CA) in which expression of EP2C-VP16 is inducible, as described in Zhang *et al.*, *supra*. To generate reporter constructs, three tandem copies of the EP2C target site, or its variants (see Figure 4B, column 2), were inserted between the Mlu I and BglII sites of the pGL3 luciferase-encoding vector (Promega, Madison, WI), upstream of the SV40 promoter. Structures of all reporter constructs were confirmed by DNA sequencing.

Luciferase reporter assays were performed by co-transfection of luciferase reporter construct (200 ng) and pCMV- β gal (100 ng, used as an internal control) into the EP2C cells seeded in 6-well plates. Expression of the EP2C-VP16 transcriptional activator was induced with doxycycline (0.05 μ g/ml) 24 h after transfection of reporter constructs. Cell lysates were harvested 40 hours post-transfection, luciferase and β -galactosidase activities were measured by the Dual-Light Reporter Assay System (Tropix, Bedford, MA), and luciferase activities were normalized to the co-transfected β -galactosidase activities. The results, shown on the right side of Figure 4B, showed that the normalized luciferase activity for each reporter construct was well correlated with the *in vitro* binding affinity of EP2C to the target sequence present in the construct. For example, the target sequences to which EP2C bound with greatest affinity (2C0 and 2C2, K_d of 2 nM for each) both stimulated the highest levels of luciferase activity, when used to drive luciferase expression in the reporter construct (Figure 4B). Target sequences to which EP2C bound with 2-fold lower affinity, 2C1 and 2C5 (K_d of 4 nM for each),

stimulated roughly half the luciferase activity of the 2C0 and 2C2 targets. The 2C3 and 2C4 sequences, for which EP2C showed the lowest *in vitro* binding affinities, also yielded the lowest levels of *in vivo* activity when used to drive luciferase expression.

5 Target 3B, a sequence to which EP2C does not bind, yielded background levels of luciferase activity, similar to those obtained with a luciferase-encoding vector lacking EP2C target sequences (pGL3). Thus there exist good correlations between binding affinity (as determined by K_d measurement), binding specificity (as determined by site selection) and *in vivo* functionality for engineered zinc finger proteins.

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FOUO "SECRET"

TABLE 1

<u>SBS#</u>	<u>TARGET</u>	SEQ ID	<u>F1</u>	SEQ ID	<u>F2</u>	SEQ ID	<u>F3</u>	SEQ ID	<u>Kd</u> (nM)
249	GCGGGGGCG	17	RSDELTR	123	RSDHLSR	229	RSDELRR	335	20
250	GCGGGGGCG	18	RSDELTR	124	RSDHLSR	230	RSDTLKK	336	70
251	GCGGAGGCG	19	RSDELTR	125	RSDNLTR	231	RSDELRR	337	27.5
252	GCGGCCGCG	20	RSDELTR	126	DRSSLTR	232	RSDELRR	338	100
253	GGATGGGGG	21	RSDHLAR	127	RSDHLTT	233	QRAHLAR	339	0.75
256	GCGGGGTCC	22	ERGDLTT	128	RSDHLSR	234	RSDELRR	340	800
258	GCGGGCGGG	23	RSDHLTR	129	ERGHLTR	235	RSDELRR	341	15
259	GCAGAGGAG	24	RSDNLAR	130	RSDNLAR	236	QSGSLTR	342	250
261	GAGGTGGCC	25	ERGTLAR	131	RSDALSR	237	RSDNLSR	343	0.5
262	GCGGGGGCT	26	QSSDLQR	132	RSDHLSR	238	RSDELRR	344	20
263	GCGGGGGCT	27	QSSDLQR	133	RSDHLSR	239	RSDTLKK	345	1
264	GTGGCTGCC	28	DRSSLTR	134	QSSDLQR	240	RSDALAR	346	27
265	GTGGCTGCC	29	ERGTLAR	135	QSSDLQR	241	RSDALAR	347	600
269	GGGGCCGGG	30	RSDHLTR	136	DRSSLTR	242	RSDHLTR	348	5
270	GGGGCCGGG	31	RSDHLTR	137	ERGTLAR	243	RSDHLTR	349	52.5
272	GCAGGGGCC	32	DRSSLTR	138	RSDHLSR	244	QSGSLTR	350	20
337	TGCGGGGCAA	33	RSADLTR	139	RSDHLTR	245	ERQHLAT	351	24
338	TGCGGGGCAA	34	RSADLTR	140	RSDHLTR	246	ERDHLRT	352	8
339	TGCGGGGCAA	35	RSADLTR	141	RSDHLTT	247	ERQHLAT	353	64
340	TGCGGGGCAA	36	RSADLTR	142	RSDHLTT	248	ERDHLRT	354	48
341	TGCGGGGCAA	37	RSADLTR	143	RGDHLKD	249	ERQHLAT	355	1000
342	TGCGGGGCAA	38	RSADLTR	144	RGDHLKD	250	ERDHLRT	356	1000
343	TGCGGGGCAA	39	QSGSLTR	145	RSDHLTR	251	ERQHLAT	357	8
344	TGCGGGGCAA	40	QSGSLTR	146	RSDHLTR	252	ERDHLRT	358	6

345	TGCGGGGCAA	41	QSGSLTR	147	RSDHLTT	253	ERQHLAT	359	96
346	TGCGGGGCAA	42	QSGSLTR	148	RSDHLTT	254	ERDHLRT	360	64
347	TGCGGGGCAA	43	QSGSLTR	149	RGDHLKD	255	ERQHLAT	361	1000
348	TGCGGGGCAA	44	QSGSLTR	150	RGDHLKD	256	ERDHLRT	362	1000
367	GGGGGCGGG	45	RSDHLTR	151	DSGHLTR	257	RSDHLQR	363	60
368	GAGGGGGCG	46	RSEDLTR	152	RSDHLTR	258	RSDNLTR	364	3.5
369	GTAGTTGTG	47	RSDALTR	153	TGGSLAR	259	QSGSLTR	365	95
370	GTAGTTGTG	48	RSDALTR	154	NRATLAR	260	QSASLTR	366	300
371	GTAGTTGTG	49	RSDALTR	155	NRATLAR	261	QSGSLTR	367	175
372	GTAGTTGTG	50	RSDSLLR	156	TGGSLAR	262	QSASLTR	368	112.5
373	GTAGTTGTG	51	RSDSLLR	157	NRATLAR	263	QSASLTR	369	320
374	GCTGAGGAA	52	QRSNLVR	158	RSDNLTR	264	TSSELQR	370	3.3
375	GAGGAAGAT	53	QQSNLAR	159	QSGNLQR	265	RSDNLTR	371	85
401	GTAGTTGTG	54	RSDALTR	160	TGGSLAR	266	QSASLTR	372	80
403	GTAGTTGTG	55	RSDSLLR	161	NRATLAR	267	QSGSLTR	373	750
421	GTAGTTGTG	56	DSDSLLR	162	TGGSLAR	268	QSGSLTR	374	500
422	GTAGTTGTG	57	RSDSLLR	163	TGGSLTR	269	QSGSLTR	375	200
423	GTAGTTGTG	58	RSDALTR	164	TGGSLAR	270	QRSALAR	376	1000
424	GATGCTGAG	59	RSDNLTR	165	TSSELQR	271	TSANLSR	377	100
425	GATGCTGAG	60	RSDNLTR	166	QSSDLQR	272	QQSNLAR	378	25
426	GATGCTGAG	61	RSDNLTR	167	QSSDLQR	273	TSANLSR	379	5.5
427	GCTGAGGAA	62	QRSNLVR	168	RSDNLTR	274	QSSDLQR	380	1
428	GAAGATGAC	63	DSSNLTR	169	QQSNLAR	275	QRSNLVR	381	120
429	GAAGATGAC	64	DSSNLTR	170	TSANLSR	276	QRSNLVR	382	50
430	GATGACGAC	65	EKANLTR	171	DSSNLTR	277	QQSNLAR	383	250
431	GACGACGGC	66	DSGHLTR	172	DRSNLER	278	DSSNLTR	384	100
432	GACGACGGC	67	DSGHLTR	173	DHANLAR	279	DSSNLTR	385	1000
433	GACGACGGC	68	DSGNLTR	174	DHANLAR	280	DSSNLTR	386	1000
434	GACGGCGTA	69	QSASLTR	175	DSGHLTR	281	EKANLTR	387	152.5
435	GACGGCGTA	70	QSASLTR	176	DSGHLTR	282	ERGNLTR	388	150
436	GACGGCGTA	71	QRSALAR	177	DSGHLTR	283	EKANLTR	389	95

437	GACGGCGTA	72	QRSALAR	178	DSGHLTR	284	ERGNLTR	390	117.5
438	GAGGGGGCG	73	RSDELTR	179	RSDHLTT	285	RSDNLTR	391	62.5
440	GCCGAGGTGC	74	RSDSLLR	180	RSKNLQR	286	ERGTLAR	392	40
441	GGTGGAGTCA	75	DSGSLTR	181	QSGHLQR	287	TSGHLTR	393	250
445	GTCGCAGTGA	76	RSDSLRR	182	QSSDLQK	288	DSGSLTR	394	1000
450	GACTTGGTGC	77	RSDTLAR	183	RGDALTS	289	DRSNLTR	395	130
453	GGTGGAGTCA	78	DRSALAR	184	QSGHLQR	290	DSSKLSR	396	150
461	GAGTACTGTA	79	QRSHLTT	185	DRSNLRT	291	RSDNLAR	397	120
463	GTGGAGGAGA	80	RSDNLTR	186	RSDNLAR	292	RSDALAR	398	0.5
464	GTGGAGGAGA	81	RSDNLTR	187	RSDNLAR	293	RSDSLAR	399	0.4
466	CAGGCTGCGC	82	RSDDLTR	188	QSSDLQR	294	RSDNLRE	400	65
467	CAGGCTGCGC	83	RSDELTR	189	QSSDLQR	295	RGDHLKD	401	800
468	CAGGCTGCGC	84	RSDDLTR	190	QSSDLQR	296	RGDHLKD	402	42
469	GAAGAGGTCT	85	DRSALAR	191	RSDNLAR	297	QSGNLTR	403	13.5
472	GAGGTCTGGA	86	RSSHITT	192	DRSALAR	298	RSDNLAR	404	80
476	GGAGAGGATG	87	TTSNLRR	193	RSDNLAR	299	QSDHLTR	405	80
477	GGAGAGGATG	88	TTSNLRR	194	RSDNLAR	300	QRAHLAR	406	100
478	GGAGAGGATG	89	TTSNLRR	195	RSDNLAR	301	QSGHLRR	407	60
479	GTGGCGGACC	90	DSSNLTR	196	RSDELQR	302	RSDALAR	408	8.5
480	GTGGCGGACC	91	DSSNLTR	197	RADTLRR	303	RSDALAR	409	5
483	GAGGGCGAAG	92	QSANLAR	198	ESSKLKR	304	RSDNLAR	410	130
484	GAGGGCGAAG	93	QSDNLAR	199	ESSKLKR	305	RSDNLAR	411	1000
485	GGAGAGGTTT	94	QSSALAR	200	RSDNLAR	306	QRAHLAR	412	110
487	GGAGAGGTTT	95	NRATLAR	201	RSDNLAR	307	QSGHLAR	413	76.9
488	TGGTAGGGGG	96	RSDHLAR	202	RSDNLTT	308	RSDHLTT	414	35
490	TAGGGGGTGG	97	RSDSLLR	203	RSDHLTR	309	RSDNLTT	415	1.5
503	GCCGAGGTGC	98	RSDSLLR	204	RSDNLAR	310	ERGTLAR	416	50
504	GCCGAGGTGC	99	RSDSLLR	205	RSDNLAR	311	DRSDLTR	417	25
505	GCCGAGGTGC	100	RSDSLLR	206	RSDNLAR	312	DCRDLAR	418	65
526	GCGGGCGGGC	101	RSDHLTR	207	ERGHLTR	313	RSDTLKK	419	8
543	GAGTGTGTGA	102	RSDLLQR	208	MSHHLKE	314	RSDHLRS	420	50

544	GAGTGTGTGA	103	RSDSLLR	209	MSHHLKE	315	RSDNLAR	421	125
545	GAGTGTGTGA	104	RKDSLVR	210	TSDHLAS	316	RSDNLTR	422	32
546	GAGTGTGTGA	105	RSDLLQR	211	MSHHLKT	317	RLDGLRT	423	500
547	GAGTGTGTGA	106	RKDSLVR	212	TSGHLTS	318	RSDNLTR	424	500
548	GAGTGTGTGA	107	RSSLLQR	213	MSHHLKT	319	RSDHLSR	425	500
549	GAGTGTGTGA	108	RSSLLQR	214	MSHHLKE	320	RSDHLSR	426	500
550	GAGTGTGTGA	109	RKDSLVR	215	TKDHLAS	321	RSDNLTR	427	20
551	GAGTGTGTGA	110	RSDLLQR	216	MSHHLKT	322	RSDHLSR	428	50
552	GAGTGTGTGA	111	RKDSLVR	217	MSHHLKT	323	RSDNLTR	429	31
553	GAGTGTGTGA	112	RSDSLLR	218	MSHHLKE	324	RSDNLTR	430	125
554	GAGTGTGTGA	113	RKDSLVR	219	TSDHLAS	325	RSDNLAR	431	62.5
558	TGCGGGGCA	114	QSGDLTR	220	RSDHLTR	326	DSGHLAS	432	21
559	GAGTGTGTGA	115	RSDSLLR	221	TSDHLAS	327	RSDNLAR	433	1000
560	GAGTGTGTGA	116	RSSLLQR	222	MSHHLKT	328	RSDHLSR	434	500
561	GAGTGTGTGA	117	RKDSLVR	223	MSHHLKE	329	RSDNLAR	435	1000
562	GAGTGTGTGA	118	RSDSLLR	224	TSGHLTS	330	RSDNLAR	436	1000
565	GATGCTGAG	119	RSDNLTR	225	TSSELQR	331	QQSNLAR	437	100
567	GAAGATGAC	120	EKANLTR	226	TSANLSR	332	QRSNLVR	438	47.5
568	GATGACGAC	121	EKANLTR	227	DSSNLTR	333	TSANLSR	439	300
569	GTAGTTGTG	122	RSDSLLR	228	TGGSLAR	334	QRSALTR	440	52

TABLE 2

<u>SBS#</u>	<u>TARGET</u>	<u>SEQ</u> <u>ID</u>	<u>F1</u>	<u>SEQ</u> <u>ID</u>	<u>F2</u>	<u>SEQ</u> <u>ID</u>	<u>F3</u>	<u>SEQ</u> <u>ID</u>	<u>Kd</u> <u>(nM)</u>
201	GCAGCCTTG	441	RSDSLTS	646	ERSTLTR	851	QRADLRR	1056	1000
202	GCAGCCTTG	442	RSDSLTS	647	ERSTLTR	852	QRADLAR	1057	1000
203	GCAGCCTTG	443	RSDSLTS	648	ERSTLTR	853	QRATLRR	1058	1000
204	GCAGCCTTG	444	RSDSLTS	649	ERSTLTR	854	QRATLAR	1059	1000
205	GAGGTAGAA	445	QSANLAR	650	QSATLAR	855	RSDNLSR	1060	80
206	GAGGTAGAA	446	QSANLAR	651	QSAVLAR	856	RSDNLSR	1061	1000
207	GAGTGGTTA	447	QRASLAS	652	RSDHLTT	857	RSDNLAR	1062	70
208	TAGGTCTTA	448	QRASLAS	653	DRSALAR	858	RSDNLAS	1063	1000
209	GGAGTGGTT	449	QSSALAR	654	RSDALAR	859	QRAHLAR	1064	35
210	GGAGTGGTT	450	NRDTLAR	655	RSDALAR	860	QRAHLAR	1065	65
211	GGAGTGGTT	451	QSSALAR	656	RSDALAS	861	QRAHLAR	1066	140
212	GGAGTGGTT	452	NRDTLAR	657	RSDALAS	862	QRAHLAR	1067	400
213	GTTGCTGGA	453	QRAHLAR	658	QSSTLAR	863	QSSALAR	1068	1000
214	GTTGCTGGA	454	QRAHLAR	659	QSSTLAR	864	NRDTLAR	1069	1000
215	GAAGTCTGT	455	NRDHLMV	660	DRSALAR	865	QSANLSR	1070	1000
216	GAAGTCTGT	456	NRDHLTT	661	DRSALAR	866	QSANLSR	1071	1000
217	GAGGTCGTA	457	QRSALAR	662	DRSALAR	867	RSDNLAR	1072	40
219	GATGTTGAT	458	QQSNLAR	663	NRDTLAR	868	NRDNLSR	1073	1000
220	GATGTTGAT	459	QQSNLAR	664	NRDTLAR	869	QQSNLSR	1074	1000
221	GATGAGTAC	460	DRSNLRT	665	RSDNLAR	870	NRDNLAR	1075	1000
222	GATGAGTAC	461	ERSNLRT	666	RSDNLAR	871	NRDNLAR	1076	1000
223	GATGAGTAC	462	DRSNLRT	667	RSDNLAR	872	QQSNLAR	1077	105
224	GATGAGTAC	463	ERSNLRT	668	RSDNLAR	873	QQSNLAR	1078	1000
225	TGGGAGGTC	464	DRSALAR	669	RSDNLAR	874	RSDHLTT	1079	6
226	GCAGCCTTG	465	RGDALTS	670	ERGTTLAR	875	QSGSLTR	1080	1000
227	GCAGCCTTG	466	RGDALTV	671	ERGTTLAR	876	QSGSLTR	1081	1000

228	GCAGCCTTG	467	RGDALTM	672	ERGTLLAR	877	QSGSLTR	1082	1000
229	GCAGCCTTG	468	RGDALTS	673	ERGTLLAR	878	RSDELTR	1083	1000
230	GCAGCCTTG	469	RGDALTV	674	ERGTLLAR	879	RSDELTR	1084	1000
231	GCAGCCTTG	470	RGDALTM	675	ERGTLLAR	880	RSDELTR	1085	1000
232	GGTGTGGTG	471	RSDALTR	676	RSDALAR	881	NRSHLAR	1086	50
233	GGTGTGGTG	472	RSDALTR	677	RSDALAR	882	QASHLAR	1087	100
235	GTAGAGGTG	473	RSDALTR	678	RSDNLAR	883	QRGALAR	1088	80
236	GGGGAGGGG	474	RSDHLAR	679	RSDNLAR	884	RSDHLSR	1089	0.3
237	GGGGAGGCC	475	ERGTLLAR	680	RSDNLAR	885	RSDHLSR	1090	0.3
238	GGGGAGGCC	476	ERGTLLAR	681	RSDNLQR	886	RSDHLSR	1091	0.8
239	GGCGGGGAG	477	RSDNLTR	682	RSDHLTR	887	DRSHLAR	1092	0.4
240	GCAGGGGAG	478	RSDNLTR	683	RSDHLSR	888	QSGSLTR	1093	1
242	GGGGGTGCT	479	QSSDLRR	684	QSSHLAR	889	RSDHLSR	1094	1
243	GTGGGCGCT	480	QSSDLRR	685	DRSHLAR	890	RSDALAR	1095	75
244	TAAGAAGGG	481	RSDHLAR	686	QSGNLTR	891	QSGNLRT	1096	100
245	TAAGAAGGG	482	RSDHLAR	687	QSANLTR	892	QSGNLRT	1097	235
246	GAAGGGGAG	483	RSDNLAR	688	RSDHLAR	893	QSGNLTR	1098	2
247	GAAGGGGAG	484	RSDNLAR	689	RSDHLAR	894	QSGNLRR	1099	2
276	GCGGCCGCG	485	RSDELTR	690	ERGTLLAR	895	RSDEKTR	1100	90
277	GCGGCCGCG	486	RSDELTR	691	DRSSLTR	896	RSDEKTR	1101	107
278	GCGGCCGCG	487	QSWELTR	692	ERGTLLAR	897	RSDEKTR	1102	190
279	GCGGCCGCG	488	QSWELTR	693	DRSSLTR	898	RSDEKTR	1103	260
280	GCGGCCGCG	489	QSGSLTR	694	ERGTLLAR	899	RSDEKTR	1104	160
281	GCGGCCGCG	490	QSGSLTR	695	DRSSLTR	900	RSDEKTR	1105	225
282	GCAGAAGTG	491	RGDALTR	696	QSANLTR	901	QSADLAR	1106	1000
283	GCAGAAGTG	492	RSDALTR	697	QSGNLTR	902	QSGSLTR	1107	2
284	GCGGCCGCG	493	QSGSLTR	698	RSDHLTT	903	RSDEKTR	1108	1000
285	TGTGCGGCC	494	ERGTLLAR	699	RSDELTR	904	SRDHLQS	1109	1000
287	GCAGAAGCG	495	RGPDLAR	700	QSANLTR	905	QSGSLTR	1110	1000
288	GCAGAAGCG	496	RGPDLAR	701	QSANLTR	906	QSGSLTR	1111	1000
289	GCAGAAGCG	497	RGPDLAR	702	QSGNLQR	907	QSGSLTR	1112	800

290	GCAGAAGCG	498	RSDELAR	703	QSANLQR	908	QSADLAR	1113	1000
292	GCAGAAGCG	499	RSDELTR	704	QSANLQR	909	QSGSLTR	1114	1000
293	GTGTGCGGC	500	DRSHLTR	705	ERHSLQT	910	RSDALTR	1115	320
296	TGCGCGGCC	501	ERGTLAR	706	RSDELTR	911	DRDHLQS	1116	1000
297	TGCGCGGCC	502	ERGTLAR	707	RSDELRR	912	DRSHLQT	1117	500
298	GCTTAGGCA	503	QTGELRR	708	RSDNLQK	913	TSGDLSR	1118	4000
299	GCTTAGGCA	504	QTSDLRR	709	RSDNLQK	914	QSSDLQR	1119	4000
300	GCTTAGGCA	505	QTADLRR	710	RSDNLQR	915	QSSDLSR	1120	400
301	GCTTAGGCA	506	QSADLRR	711	RSDNLQT	916	QSSDLSR	1121	350
302	GCTTAGGCA	507	QSGSLTR	712	RSDNLQT	917	QSSDLSR	1122	75
303	GCTTAGGCA	508	QTGSLTR	713	RSDNLQT	918	QSSDLSR	1123	135
304	GCTTAGGCA	509	QTADLTR	714	RSDNLQT	919	QSSDLSR	1124	230
305	GCTTAGGCA	510	QTGDLTR	715	RSDNLQT	920	QSSDLSR	1125	230
306	GCTTAGGCA	511	QTASLTR	716	RSDNLQT	921	QSSDLSR	1126	280
307	GAAGAAGCG	512	RSDELRR	717	QSGNLQR	922	QSGNLSR	1127	50.5
308	GAAGAAGCG	513	RSDELRR	718	QSANLQR	923	QSANLQR	1128	1000
309	GGAGATGCC	514	ERSDLRR	719	QSSNLQR	924	QSGHLSR	1129	4000
310	GGAGATGCC	515	DRSDLTR	720	NRDNLQT	925	QSGHLSR	1130	1000
311	GGAGATGCC	516	DRSTLTR	721	NRDNLQR	926	QSGHLSR	1131	170
312	GGAGATGCC	517	ERGTLAR	722	NRDNLQR	927	QSGHLSR	1132	2000
313	GGAGATGCC	518	DRSDLTR	723	QRSNLQR	928	QSGHLSR	1133	1000
314	GGAGATGCC	519	DRSSLTR	724	QSSNLQR	929	QSGHLSR	1134	117.5
315	GGAGATGCC	520	ERGTLAR	725	QSSNLQR	930	QSGHLSR	1135	265
316	GGAGATGCC	521	ERGTLAR	726	QRDNLQR	931	QSGHLSR	1136	3000
318	TAGGAGATGC	522	RSDALTS	727	RSDNLAR	932	RSDNLAS	1137	100
319	GGGGAAGGG	523	KTSHLRA	728	QSGNLSR	933	RSDHLSR	1138	125
320	GGGGAAGGG	524	RSDHLTR	729	QSGNLSR	934	RSDHLSR	1139	5
321	GGCGGAGAT	525	TTSNLRR	730	QSGHLQR	935	DRSHLTR	1140	200
323	GGCGGAGAT	526	TTSNLRR	731	QSGHLQR	936	DRDHLTR	1141	600
324	GGCGGAGAT	527	TTSNLRR	732	QSGHLQR	937	DRDHLTR	1142	200
325	GTATCTGCT	528	NSSDLTR	733	NSDVLTS	938	QSDVLTR	1143	1000

326	GTATCTGTT	529	NSDALTR	734	NSDVLTS	939	QSDVLTR	1144	1000
327	TCTGCTGGG	530	RSDHLTR	735	NSADLTR	940	NSDDLTR	1145	1000
328	TCTGTTGGG	531	RSDHLTR	736	NSSALTS	941	NSDDLTR	1146	1000
349	GGTGTCGCC	532	DCRDLAR	737	DSGSLTR	942	TSGHLTR	1147	1000
350	TCCGAGGGT	533	TSGHLTR	738	RSDNLTR	943	DCRDLTT	1148	332
351	GCTGGTGTC	534	DSGSLTR	739	TSGHLTR	944	TLHTLTR	1149	1000
352	GGAGGGGTG	535	RSDSLLR	740	RSDHLTR	945	QSDHLTR	1150	26
353	GTTGGAGCC	536	DCRDLAR	741	QSDHLTR	946	TSGALTR	1151	1000
354	GAAGAGGAC	537	DSSNLTR	742	RSDNLTR	947	QRSNLVR	1152	28
355	GAAGAGGAC	538	EKANLTR	743	RSDNLTR	948	QRSNLVR	1153	20
356	GGCTGGGCG	539	RSDELRR	744	RSDHLTK	949	DSDHLSR	1154	1000
357	GGCTGGGCG	540	RSDELRR	745	RSDHLTK	950	DSDHLSR	1155	1000
358	GGCTGGGCG	541	RSDELRR	746	RSDHLTK	951	DSSHLSR	1156	225
361	GGGTTTGGG	542	RSDHLTR	747	QSSALTR	952	RSDHLTR	1157	130
363	GGGTTTGGG	543	RSDHLTR	748	QSSVLTR	953	RSDHLTR	1158	200
364	GTGTCCGAAG	544	RSDNLTR	749	DSAVLTT	954	RSDSLTR	1159	1000
365	GGTGCTGGT	545	QASHLTR	750	QASVLTR	955	QASHLTR	1160	600
366	GAGGGTGCT	546	QASVLTR	751	QASHLTR	956	RSDNLTR	1161	1000
367	GGGGGCGGG	547	RSDHLTR	752	DSGHLTR	957	RSDHLQR	1162	60
368	GAGGGGGCG	548	RSDELTR	753	RSDHLTR	958	RSDNLTR	1163	3.5
369	GTAGTTGTG	549	RSDALTR	754	TGGSLAR	959	QSGSLTR	1164	95
370	GTAGTTGTG	550	RSDALTR	755	NRATLAR	960	QSASLTR	1165	300
371	GTAGTTGTG	551	RSDALTR	756	NRATLAR	961	QSGSLTR	1166	175
372	GTAGTTGTG	552	RSDSLLR	757	TGGSLAR	962	QSASLTR	1167	112.5
373	GTAGTTGTG	553	RSDSLLR	758	NRATLAR	963	QSASLTR	1168	320
374	GCTGAGGAA	554	QRSNLVR	759	RSDNLTR	964	TSSELQR	1169	3.3
375	GAGGAAGAT	555	QQSNLAR	760	QSGNLQR	965	RSDNLTR	1170	85
377	GTGTTGGCAG	556	QSGSLTR	761	RGDALTS	966	RSDALTR	1171	89
378	GCCGAGGAGA	557	RSDNLTR	762	RSDNLTR	967	DRSSLTR	1172	31
379	GCCGAGGAGA	558	RSDNLTR	763	RSDNLTR	968	ERGTLAR	1173	3
380	GAGTCGGAAG	559	QSANLAR	764	RSDELTT	969	RSDNLAR	1174	1000

501	GTGGGGGTT	591	NRATLAR	796	RSDHLSR	1001	RSDALAR	1206	8
502	GGGGTGGGA	592	QSAHLAR	797	RSDALAR	1002	RSDHLSR	1207	60
507	GAGGTAGAGG	593	RSDNLAR	798	QRSALAR	1003	RSDNLAR	1208	10
508	GAGGTAGAGG	594	RSDNLAR	799	QSATLAR	1004	RSDNLAR	1209	10
509	GTCGTGTGGC	595	RSDHLTT	800	RSDALAR	1005	DRSALAR	1210	100
510	GTTGAGGAAG	596	QSGNLAR	801	RSDNLAR	1006	NRATLAR	1211	100
511	GTTGAGGAAG	597	QSGNLAR	802	RSDNLAR	1007	QSSALAR	1212	100
512	GAGGTGGAAG	598	QSGNLAR	803	RSDALAR	1008	RSDNLAR	1213	10
513	GAGGTGGAAG	599	QSANLAR	804	RSDALAR	1009	RSDNLAR	1214	1.5
514	TAGGTGGTGG	600	RSDALTR	805	RSDALAR	1010	RSDNLTT	1215	10
515	TGGGAGGAGT	601	RSDNLTR	806	RSDNLTR	1011	RSDHLTT	1216	0.5
516	GGAGGAGCT	602	TTSELRR	807	QSGHLQR	1012	QSGHLSR	1217	700
517	GGAGCTGGGG	603	RTDHLRR	808	TSSELQR	1013	QSGHLSR	1218	50
518	GGGGGAGGAG	604	QTGHLRR	809	QSGHLQR	1014	RSDHLSR	1219	30
519	GGGGAGGAGA	605	RSDNLAR	810	RSDNLSR	1015	RSDHLSR	1220	0.3
520	GGAGGAGAT	606	TTANLRR	811	QSGHLQR	1016	QSGHLSR	1221	300
521	GCAGCAGGA	607	QTGHLRR	812	QSGELQR	1017	QSGELSR	1222	1000
522	GATGAGGCA	608	QTGELRR	813	RSDNLQR	1018	TSANLSR	1223	200
527	GGGGAGGATC	609	TTSNLRR	814	RSSNLQR	1019	RSDHLSR	1224	2
528	GGGGAGGATC	610	TTSNLRR	815	RSSNLQR	1020	RSDHLSR	1225	10
529	GAGGCTTGGG	611	RTDHLRK	816	TSAELQR	1021	RSSNLSR	1226	1000
531	GCGGAGGCTT	612	TTGELRR	817	RSSNLQR	1022	RSDELSR	1227	160
532	GCGGAGGCTT	613	QSSDLQR	818	RSSNLQR	1023	RSDELSR	1228	100
533	GCGGAGGCTT	614	QSSDLQR	819	RSDNLAR	1024	RSADLSR	1229	7
534	GCGGAGGCTT	615	QSSDLQR	820	RSDNLAR	1025	RSDDLRR	1230	10
535	GCAGCCGGG	616	RTDHLRR	821	ESSDLQR	1026	QSGELSR	1231	1000
538	GCAGAGGCTT	617	QSSDLQR	822	RSDNLAR	1027	QSGSLTR	1232	70
540	TGGGCAGGCC	618	DRSHLTR	823	QSGSLTR	1028	RSDHLTT	1233	55
541	GGGGAGGAT	619	TTSNLRR	824	RSSNLQR	1029	RSDHLSR	1234	3
570	GGGGAAGGCT	620	DSGHLTR	825	QRSNLVR	1030	RSDHLTR	1235	20
571	GTGTGTGTGT	621	RSDSLTR	826	QRSNLVR	1031	RSDSLLR	1236	1000

572	GCATACGTGG	622	RSDSLLR	827	DKGNLQS	1032	QSDDLTR	1237	1000
573	GCATACGTG	623	RSDSLLR	828	DKGNLQS	1033	QSGDLTR	1238	1000
574	TACGTGGGGT	624	RSDHLTR	829	RSDHLTR	1034	DKGNLQT	1239	25
575	TACGTGGGCT	625	DFSHLTR	830	RSDHLTR	1035	DKGNLQT	1240	472
576	GAGGGTGTTG	626	NSDTLAR	831	TSGLHLTR	1036	RSDNLTR	1241	200
577	GGAGCGGGGA	627	RSDHLR	832	RSDELQR	1037	QSDHLTR	1242	200
579	GGGGTTGAGG	628	RSDNLTR	833	NRDTLAR	1038	TSGLHLTR	1243	200
580	GGTGTGAG	629	QRAHLAR	834	NRDTLAR	1039	TSGLHLTR	1244	1000
581	TACGTGGGTT	630	QSSHLTR	835	RSDSLLR	1040	DKGNLQT	1245	382
583	GTAGGGGTTG	631	NSSALTR	836	RSDHLTR	1041	QSASLTR	1246	46
584	GAAGGCGGAG	632	QAGHLTR	837	DKSHLTR	1042	QSGNLTR	1247	1000
585	GAAGGCGGAG	633	QAGHLTR	838	DSGLHLTR	1043	QSGNLTR	1248	1000
587	GGGGGTTACG	634	DKGNLQT	839	TSGLHLTR	1044	RSDHLSK	1249	500
588	GGGGGGGGGG	635	RSDHLR	840	RSDHLTR	1045	RSDHLSK	1250	30
589	GGAGTATGCT	636	DSGLHAS	841	QSATLAR	1046	QSDHLTR	1251	1000
595	TGGTTGGTAT	637	QRGSLAR	842	RGDALTR	1047	RSDHLTT	1252	73.3
597	TGGTTGGTA	638	QNSAMRK	843	RGDALTS	1048	RSDHLTT	1253	1000
598	TGGTTGGTA	639	QRGSLAR	844	RDGSLTS	1049	RSDHLTT	1254	1000
599	TGGTTGGTA	640	QNSAMRK	845	RDGSLTS	1050	RSDHLTT	1255	1000
600	GAGTCGAA	641	QSANLAR	846	RSDELRT	1051	RSDNLAR	1256	206.7
601	GAGTCGAA	642	RSANLTR	847	RLDGLRT	1052	RSDNLAR	1257	606.7
602	GAGTCGAA	643	RSANLTR	848	RQDTLVG	1053	RSDNLAR	1258	616.7
603	GAGTCGAA	644	QSGNLAR	849	RSDELRT	1054	RSDNLAR	1259	166.7
606	GGGGAGGATC	645	TTSNLRR	850	RSDNLQR	1055	RSDHLR	1260	0.2

TABLE 3

<u>SBS#</u>	<u>TARGET</u>	<u>SEQ</u> <u>ID</u>	<u>SEQ</u> <u>F1</u> <u>ID</u>	<u>SEQ</u> <u>F2</u> <u>ID</u>	<u>SEQ</u> <u>F3</u> <u>ID</u>	<u>Kd</u> <u>(nM)</u>
897	GAGGAGGTGA	1261	RSDALAR 1347	RSDNLAR 1433	RSDNLVR 1519	0.07
828	GCGGAGGACC	1262	EKANLTR 1348	RSDNLAR 1434	RSDERKR 1520	0.1
884	GAGGAGGTGA	1263	RSDSLTR 1349	RSDNLAR 1435	RSDNLVR 1521	0.15
817	GAGGAGGTGA	1264	RSDSLTR 1350	RSDNLAR 1436	RSDNLAR 1522	0.31
666	GCGGAGGCGC	1265	RSDDLTR 1351	RSDNLTR 1437	RSDTLKK 1523	0.5
829	GCGGAGGACC	1266	EKANLTR 1352	RSDNLAR 1438	RSDTLKK 1524	0.52
670	GACGTGGAGG	1267	RSDNLAR 1353	RSDALAR 1439	DRSNLTR 1525	0.57
801	AAGGAGTCGC	1268	RSADLRT 1354	RSDNLAR 1440	RSDNLTQ 1526	0.85
668	GTGGAGGCCA	1269	ERGTLAR 1355	RSDNLAR 1441	RSDALAR 1527	1.13
895	ATGGATTCAG	1270	QSHDLTK 1356	TSGNLVR 1442	RSDALTQ 1528	1.4
799	GGGGGAGCTG	1271	QSSDLQR 1357	QRAHLER 1443	RSDHLR 1529	1.85
798	GGGGGAGCTG	1272	QSSDLQR 1358	QSGHLQR 1444	RSDHLR 1530	3
842	GAGGTGGGCT	1273	DRSHLTR 1359	RSDALAR 1445	RSDNLAR 1531	5.4
894	TCAGTGGTAT	1274	QRSALAR 1360	RSDALSR 1446	QSHDLTK 1532	6.15
892	ATGGATTCAG	1275	QSHDLTK 1361	QGSNLVR 1447	RSDALTQ 1533	6.2
888	TCAGTGGTAT	1276	QSSSLVR 1362	RSDALSR 1448	QSHDLTK 1534	14
739	GCGGGCGGGC	1277	RSDHLTR 1363	ERGHLTR 1449	RSDDLRR 1535	16.5
850	CAGGCTGTGG	1278	RSDALTR 1364	QSSDLTR 1450	RSDNLRE 1536	17
797	GCAGAGGCTG	1279	QSSDLQR 1365	RSDNLAR 1451	QSGDLTR 1537	17.5
891	TCAGTGGTAT	1280	QSSSLVR 1366	RSDALSR 1452	QSGSLRT 1538	18.5
887	TCAGTGGTAT	1281	QRSALAR 1367	RSDALSR 1453	QSGDLRT 1539	23.75
672	TCGGACGTGG	1282	RSDALAR 1368	DRSNLTR 1454	RSDELRT 1540	24
836	GGGGAGGCCC	1283	ERGTLAR 1369	RSDNLAR 1455	RSDHLR 1541	24.25
674	GCGGCGTCGG	1284	RSDELRT 1370	RADTLRR 1456	RSDTLKK 1542	27.5
849	GGGGCCCTGG	1285	RSDALRE 1371	DRSSLTR 1457	RSDHLTQ 1543	29.05
825	GAATGGGCAG	1286	QSGSLTR 1372	RSDHLTT 1458	QSGNLTR 1544	37.3

673	GCGGGTGTCT	1287	DRSALAR	1373	QSSHLAR	1459	RSDTLKK	1545	48.33
848	GGGGAGGCC	1288	DRSSLTR	1374	RSDNLAR	1460	RSDHLSR	1546	49.5
662	AGAGCGGCAC	1289	QTGSLTR	1375	RSDELQR	1461	QSGHLNQ	1547	50
667	GAGTCGGACG	1290	DRSNLTR	1376	RSDELRT	1462	RSDNLAR	1548	50
803	GCAGCGGCTC	1291	QSSDLQR	1377	RSDELQR	1463	QSGSLTR	1549	57.5
671	TCGGACGAGT	1292	RSDNLAR	1378	DRSNLTR	1464	RSDELRT	1550	64
851	GAGATGGATC	1293	QSSNLQR	1379	RRDVL MN	1465	RLHNLQR	1551	74
804	GCAGCGGCTC	1294	QSSDLQR	1380	RSDDLNR	1466	QSGSLTR	1552	82.5
669	GACGAGTCGG	1295	RSDELRT	1381	RSDNLAR	1467	DRSNLTR	1553	90
682	GCTGCAGGAG	1296	RSDHLAR	1382	QSGDLTR	1468	QSSDLSR	1554	90
845	GAGATGGATC	1297	QSSNLQR	1383	RSDALRQ	1469	RLHNLQR	1555	112.5
663	AGAGCGGCAC	1298	QTGSLTR	1384	RSDELQR	1470	KNWKLQA	1556	115
738	GCGGGGTCCG	1299	ERGT LTT	1385	RSDHLSR	1471	RSDDLRR	1557	120
664	AGAGCGGCAC	1300	QTGSLTR	1386	RADTLRR	1472	ASSRLAT	1558	125
833	GACTAGGACC	1301	EKANLTR	1387	RSDNLTK	1473	DRSNLTR	1559	136
685	GCTGCAGGAG	1302	RSDHLAR	1388	QSGSLTR	1474	QSSDLSR	1560	150
835	TAGGGAGCGT	1303	RADTLRR	1389	QSGHLTR	1475	RSDNLTT	1561	150
847	TAGGGAGCGT	1304	RSDDLTR	1390	QSGHLTR	1476	RSDNLTT	1562	150
818	GAATGGGCAG	1305	QSGSLTR	1391	RSDHLTT	1477	QSSNLVR	1563	167
834	GACTAGGACC	1306	EKANLTR	1392	RSDHLTT	1478	DRSNLTR	1564	186
837	GGGGCCCTGG	1307	RSDALRE	1393	DRSSLTR	1479	RSDHLSR	1565	222
764	GCAGAGGCTG	1308	TSGELVR	1394	RSDNLAR	1480	QSGDLTR	1566	255
774	GCAGCGGTAG	1309	QRSALAR	1395	RSDELQR	1481	QSGDLTR	1567	258
765	GCCGAGGCCG	1310	ERGT LAR	1396	RSDNLAR	1482	ERGT LAR	1568	262.5
766	GCCGAGGCCG	1311	ERGT LAR	1397	RSDNLAR	1483	DRSDLTR	1569	262.5
775	GCAGCGGTAG	1312	QSGALTR	1398	RSDELQR	1484	QSGDLTR	1570	265
763	GCAGAGGCTG	1313	TSGELVR	1399	RSDNLAR	1485	QSGSLTR	1571	275
838	GGGGCCCTGG	1314	RSDALRE	1400	DRSSLTR	1486	RSDHLTA	1572	300
841	GAGTGTGAGG	1315	RSDNLAR	1401	QSSHLAS	1487	RSDNLAR	1573	300
770	TTGGCAGCCT	1316	DRSSLTR	1402	QSGSLTR	1488	RSDSLTK	1574	325
767	GGGGGAGCTG	1317	QSSDLAR	1403	QSGHLQR	1489	RSDHLSR	1575	335

800	TTGGCAGCCT 1318	ERGTLLAR 1404	QSGSLTR 1490	RSDSLTK 1576	400
832	GACTAGGACC 1319	EKANLTR 1405	RSDNLTT 1491	DRSNLTR 1577	408
844	GAGATGGATC 1320	QSSNLQR 1406	RSDALRQ 1492	RSDNLQR 1578	444
683	GCTGCAGGAG 1321	QSGHLAR 1407	QSGSLTR 1493	QSSDLR 1579	500
805	GCAGCGGTAG 1322	QRSALAR 1408	RSDELQR 1494	QSGSLTR 1580	500
839	GAGTGTGAGG 1323	RSDNLAR 1409	TSDHLAS 1495	RSDNLAR 1581	625
840	GAGTGTGAGG 1324	RSDNLAR 1410	MSHHLKT 1496	RSDNLAR 1582	625
830	GGAGAGTCGG 1325	RSDELRT 1411	RSDNLAR 1497	QRAHLAR 1583	683
831	GGAGAGTCGG 1326	RSDDLTK 1412	RSDNLAR 1498	QRAHLAR 1584	700
684	GCTGCAGGAG 1327	RSAHLAR 1413	QSGSLTR 1499	QSSDLR 1585	850
846	GAGATGGATC 1328	QSSNLQR 1414	RRDVLMM 1500	RSDNLQR 1586	889.5
819	AAGTAGGGTG 1329	QSSHLTR 1415	RSDNLTT 1501	RSDNLQ 1587	1000
820	ACGGTAGTTA 1330	QSSALTR 1416	QRSALAR 1502	RSDTLQ 1588	1000
821	ACGGTAGTTA 1331	NRATLAR 1417	QRSALAR 1503	RSDTLQ 1589	1000
822	GTGTGCTGGT 1332	RSDHLTT 1418	ERQHLAT 1504	RSDALAR 1590	1000
823	GTGTGCTGGT 1333	RSDHLTK 1419	ERQHLAT 1505	RSDALAR 1591	1000
824	GTGTGCTGGT 1334	RSDHLTT 1420	DRSHLRT 1506	RSDALAR 1592	1000
885	GTGTGCTGGT 1335	RSDHLTK 1421	DRSHLRT 1507	RSDALAR 1593	1000
886	TCAGTGGTAT 1336	QSSSLVR 1422	RSDALSR 1508	QSGDLRT 1594	1000
889	ATGGATTGAT 1337	QSGSLTT 1423	QSSNLVR 1509	RSDALTQ 1595	1000
890	CTGGTATGTC 1338	QRSHLTT 1424	QRSALAR 1510	RSDALRE 1596	1000
896	AAGTAGGGTG 1339	TSGHLVR 1425	RSDNLTT 1511	RSDNLQ 1597	1000
898	ACGGTAGTTA 1340	NRATLAR 1426	QSSSLVR 1512	RSDTLQ 1598	1000
899	CTGGTATGTC 1341	QRSHLTT 1427	QSSSLVR 1513	RSDALRE 1599	1000
900	CTGGTATGTC 1342	MSHHLKE 1428	QSSSLVR 1514	RSDALRE 1600	1000
901	CTGGTATGTC 1343	MSHHLKE 1429	QRSALAR 1515	RSDALRE 1601	1000
773	GCAGCGGTAG 1344	QSGALTR 1430	RSDELQR 1516	QSGSLTR 1602	1250
768	GGGGGAGCTG 1345	QSSDLAR 1431	QRAHLER 1517	RSDHLR 1603	2000
681	GCTGCAGGAG 1346	RSAHLAR 1432	QSGDLTR 1518	QSSDLR 1604	3000

TABLE 4

<u>SBS#</u>	<u>TARGET</u>	<u>SEQ</u> <u>ID</u>	<u>F1</u>	<u>SEQ</u> <u>ID</u>	<u>F2</u>	<u>SEQ</u> <u>ID</u>	<u>F3</u>	<u>SEQ</u> <u>ID</u>	<u>Kd</u> <u>(nM)</u>
607	AAGGTGGCAG	1605	QSGDLTR	1707	RSDSLAR	1809	RLDNRTA	1911	6.5
608	TTGGCTGGGC	1606	GSWHLTR	1708	QSSDLQR	1810	RSDSLTK	1912	8
611	GTGGCTGCAG	1607	QSGDLTR	1709	QSSDLQR	1811	RSDALAR	1913	11.5
612	GTGGCTGCAG	1608	QSGTLTR	1710	QSSDLQR	1812	RSDALAR	1914	0.38
613	TTGGCTGGGC	1609	RSDHLAR	1711	QSSDLQR	1813	RGDALTS	1915	1.45
614	TTGGCTGGGC	1610	RSDHLAR	1712	QSSDLQR	1814	RSDSLTK	1916	2
616	GAGGAGGATG	1611	QSSNLQR	1713	RSDNLAR	1815	RSDNLQR	1917	0.08
617	AAGGGGGGG	1612	RSDHLSR	1714	RSDHLTR	1816	RKDNMTA	1918	1
618	AAGGGGGGG	1613	RSDHLSR	1715	RSDHLTR	1817	RKDNMTQ	1919	0.55
619	AAGGGGGGG	1614	RSDHLSR	1716	RSDHLTR	1818	RKDNMTN	1920	1.34
620	AAGGGGGGG	1615	RSDHLSR	1717	RSDHLTR	1819	RLDNRTA	1921	0.54
621	AAGGGGGGG	1616	RSDHLSR	1718	RSDHLTR	1820	RLDNRTQ	1922	0.75
624	ACGGATGTCT	1617	DRSALAR	1719	TSANLAR	1821	RSDTLRS	1923	7
628	TTGTAGGGGA	1618	RSDHLTR	1720	RSDNLTT	1822	RGDALTS	1924	130
629	TTGTAGGGGA	1619	RSSHLTR	1721	RSDNLTT	1823	RGDALTS	1925	150
630	CGGGGAGAGT	1620	RSDNLAR	1722	QSGHLQR	1824	RSDHLRE	1926	37.5
646	TTGGTGGAAG	1621	QSGNLAR	1723	RSDALAR	1825	RGDALTS	1927	35
647	TTGGTGGAAG	1622	QSANLAR	1724	RSDALAR	1826	RGDALTS	1928	40
651	GTTGTGGAAT	1623	QSGNLSR	1725	RSDALAR	1827	NRATLAR	1929	67.5
652	TAGGAGGCTG	1624	QSSDLQR	1726	RSDNLAR	1828	RSDNLTT	1930	1.5
653	TAGGAGGCTG	1625	TTSDLTR	1727	RSDNLAR	1829	RSDNLTT	1931	5.5
654	TAGGCATAAA	1626	QSGNLRT	1728	QSGSLTR	1830	RSDNLTT	1932	105
655	TAGGCATAAA	1627	QSGNLRT	1729	QSSTLRR	1831	RSDNLTT	1933	1000
656	TAGGCATAAA	1628	QSGNLRT	1730	QSGSLTR	1832	RSDNLTS	1934	540
657	TAGGCATAAA	1629	QSGNLRT	1731	QSSTLRR	1833	RSDNLTS	1935	300
660	GAGGGAGTTC	1630	NRATLAR	1732	QSGHLTR	1834	RSDNLAR	1936	8.25

661	GAGGGAGTTC	1631	TTSALTR	1733	QSGHLTR	1835	RSDNLAR	1937	1.73
665	GCGGAGGCGC	1632	RSDDVTR	1734	RSDNLTR	1836	RSDDLRR	1938	12.5
689	AAGGCGGAGA	1633	RSDNLTR	1735	RSDELQR	1837	RLDNRTA	1939	82.5
692	AAGGCGGAGA	1634	RSDNLTR	1736	RSDELQR	1838	RSDNLTQ	1940	51
693	AAGGCGGAGA	1635	RSDNLTR	1737	RADTLRR	1839	RLDNRTA	1941	95
694	AAGGCGGAGA	1636	RSDNLTR	1738	RADTLRR	1840	RSDNLTQ	1942	28.5
695	GGGGCGGAGC	1637	RSSNLTR	1739	DRSHLAR	1841	RSDHLTR	1943	850
697	TGAGCGGCGG	1638	RSDELTR	1740	RSDELSR	1842	QSGHLTK	1944	200
698	TGAGCGGCGG	1639	RSDELTR	1741	RSDELSR	1843	QSHGLTS	1945	300
699	GCGGCGGCAG	1640	QSGSLTR	1742	RSDDLQR	1844	RSDEKRR	1946	21.5
700	GCGGCGGCAG	1641	QSGDLTR	1743	RSDDLQR	1845	RSDEKRR	1947	45
701	GCAGCGGAGC	1642	RSDNLAR	1744	RSDELQR	1846	QSGSLTR	1948	50.5
702	GCAGCGGAGC	1643	RSDNLAR	1745	RSDELQR	1847	QSGDLTR	1949	73.5
704	AAGGTGGCAG	1644	QSGDLTR	1746	RSDSLAR	1848	RSDNLTQ	1950	5
705	GGGGTGGGGC	1645	RSDHLAR	1747	RSDSLAR	1849	RSDHLTR	1951	0.01
706	GGGGTGGGGC	1646	RSDHLAR	1748	RSDSLTR	1850	RSDHLTR	1952	0.05
708	GAGTCGGAA	1647	QSANLAR	1749	RQDTLVG	1851	RSDNLAR	1953	300
709	GAGTCGGAA	1648	QSANLAR	1750	RKDVLVS	1852	RSDNLAR	1954	400
710	GAGTCGGAA	1649	QSGNLAR	1751	RLDGLRT	1853	RSDNLAR	1955	400
711	GAGTCGGAA	1650	QSGNLAR	1752	RQDTLVG	1854	RSDNLAR	1956	400
712	GGTGAGGAGT	1651	RSDNLAR	1753	RSDNLAR	1855	MSDHLTR	1957	9.5
713	GGTGAGGAGT	1652	RSDNLAR	1754	RSDNLAR	1856	MSHHLTR	1958	0.15
714	TGGGTCGCGG	1653	RSDELRR	1755	DRSALAR	1857	RSDHLTT	1959	200
715	TGGGTCGCGG	1654	RADTLRR	1756	DRSALAR	1858	RSDHLTT	1960	0.46
716	TTGGGAGCAC	1655	QSGSLTR	1757	QSGHLQR	1859	RGDALTS	1961	200
717	TTGGGAGCAC	1656	QSGSLTR	1758	QSGHLQR	1860	RSDALTK	1962	150
718	TTGGGAGCAC	1657	QSGSLTR	1759	QSGHLQR	1861	RSDALTR	1963	107.5
719	GGCATGGTGG	1658	RSDALTR	1760	RSDALTS	1862	DRSHLAR	1964	20
720	GAAGAGGATG	1659	TTSNLAR	1761	RSDNLAR	1863	QSGNLTR	1965	1.6
722	ATGGGGGTGG	1660	RSDALTR	1762	RSDHLTR	1864	RSDALRQ	1966	0.7
724	GGCATGGTGG	1661	RSDALTR	1763	RSDALRQ	1865	DRSHLAR	1967	2.5

725	GCTTGAGTTA 1662	QSSALAR 1764	QSGHLQK 1866	QSSDLQR 1968	3000
726	GAAGAGGATG 1663	QSSNLAR 1765	RSDNLAR 1867	QSGNLTR 1969	1.5
727	GCGGTGGCTC 1664	QSSDLTR 1766	RSDALSR 1868	RSDTLKK 1970	0.1
728	GGTGAGGAGT 1665	RSDNLAR 1767	RSDNLAR 1869	DSSKLSR 1971	15
729	GGAGGGGAGT 1666	RSDNLAR 1768	RSDHLSR 1870	QSGHLAR 1972	1000
730	TGGGTCGCGG 1667	RSDDLTR 1769	DRSALAR 1871	RSDHLTT 1973	1000
731	GTGGGGGAGA 1668	RSDNLAR 1770	RSDHLSR 1872	RSDALAR 1974	12
732	GCGGGTGGGG 1669	RSDHLAR 1771	QSSHLAR 1873	RSDDLTR 1975	22.5
733	GCGGGTGGGG 1670	RSDHLAR 1772	QSSHLAR 1874	RSDTLKK 1976	0.32
734	GGGGCTGGGT 1671	RSDHLAR 1773	QSSDLR 1875	RSDHLSR 1977	0.25
735	GCGGTGGCTC 1672	QSSDLTR 1774	RSDALSR 1876	RSDERKR 1978	0.05
736	GAGGTGGGGA 1673	RSDHLAR 1775	RSDALSR 1877	RSDNLSR 1979	0.47
737	GGAGGGGAGT 1674	RSDNLAR 1776	RSDHLSR 1878	QRGHLR 1980	1000
740	AAGGTGGCAG 1675	QSGSLTR 1777	RSDALAR 1879	RSDNRTA 1981	12.5
741	AAGGCTGAGA 1676	RSDNLTR 1778	QSSDLQR 1880	RSDNLQ 1982	15
742	ACGGGGTTAT 1677	QRGALAS 1779	RSDHLSR 1881	RSDTLKQ 1983	29
743	ACGGGGTTAT 1678	QRGALAS 1780	RSDHLSR 1882	RSDTLQ 1984	10
744	ACGGGGTTAT 1679	QRSALAS 1781	RSDHLSR 1883	RSDTLKQ 1985	8.33
745	ACGGGGTTAT 1680	QRSALAS 1782	RSDHLSR 1884	RSDTLQ 1986	12.5
746	CTGGAAGCAT 1681	QSGSLTR 1783	QSGNLAR 1885	RSDALRE 1987	2.07
747	CTATTTTGGG 1682	RSDHLTT 1784	QSSALRT 1886	QSGALRE 1988	2000
748	TTGGACGGCG 1683	DSGHLTR 1785	DRSNLER 1887	RGDALTS 1989	112.3
749	TTGGACGGCG 1684	DRSHLTR 1786	DSSNLTR 1888	RGDALTS 1990	11.33
750	GAGGGAGCGA 1685	RSEDLTR 1787	QSAHLAR 1889	RSDNLAR 1991	52
751	GGTGAGGAGT 1686	RSDNLAR 1788	RSDNLAR 1890	NRSHLAR 1992	7
752	GAGGTGGGGA 1687	RSHHLAR 1789	RSDALSR 1891	RSDNLSR 1993	31
757	CGGGCGGCTG 1688	QSSDLRR 1790	RSEDLQR 1892	RSDHLRE 1994	14.5
758	CGGGCGGCTG 1689	QSSDLRR 1791	RADTLRR 1893	RSDHLRE 1995	16.5
759	TTGGACGGCG 1690	DSGHLTR 1792	DSSNLTR 1894	RGDALTS 1996	37
760	TTGGACGGCG 1691	DRSHLTR 1793	DRSNLER 1895	RGDALTS 1997	148.5
761	GCGGTGGCTC 1692	QSSDLQR 1794	RSDALSR 1896	RSDERKR 1998	6

762	GCGGTGGCTC	1693	QSSDLQR	1795	RSDALSR	1897	RSDTLKK	1999	18
776	ATGGACGGGT	1694	RSDHLAR	1796	DRSNLER	1898	RSDSLNQ	2000	0.4
777	ATGGACGGGT	1695	RSDHLAR	1797	DRSNLTR	1899	RSDALSA	2001	3.4
779	CGGGGAGCAG	1696	QSGSLTR	1798	QSGHLTR	1900	RSDHLAE	2002	0.5
780	CGGGGAGCAG	1697	QSGSLTR	1799	QSGHLTR	1901	RSDHLRA	2003	0.5
781	GGGGAGCAGC	1698	RSSNLRE	1800	RSDNLAR	1902	RSDHLTR	2004	4.25
783	TTGGGAGCGG	1699	RSDELTR	1801	QSGHLQR	1903	RGDALTS	2005	2000
785	TTGGGAGCGG	1700	RSDTLKK	1802	QSGHLQR	1904	RSDALTS	2006	50
786	TTGGGAGCGG	1701	RSDTLKK	1803	QSGHLQR	1905	RGDALRS	2007	2000
787	AGGGAGGATG	1702	QSDNLAR	1804	RSDNLAR	1906	RSDHLTQ	2008	4
826	GAGGGAGCGA	1703	RSDELTR	1805	QSGHLAR	1907	RSDNLAR	2009	2.75
827	GAGGGAGCGA	1704	RADTLRR	1806	QSGHLAR	1908	RSDNLAR	2010	1.2
882	GCGTGGGCGT	1705	RSDELTR	1807	RSDHLTT	1909	RSDEKRR	2011	0.01
883	GCGTGGGCGT	1706	RSDELTR	1808	RSDHLTT	1910	RSDEKRR	2012	1

TABLE 5

SBS#	TARGET	<u>SEQ</u> ID	<u>F1</u>	<u>SEQ</u> ID	<u>F2</u>	<u>SEQ</u> ID	<u>F3</u>	<u>SEQ</u> ID	<u>Kd</u> (nM)
903	ATGGAAGGG	2013	RSDHLAR	2513	QSGNLR	3013	RSDALRQ	3513	1.027
904	AAGGGTGAC	2014	DSSNLTR	2514	QSSHLAR	3014	RSDNLTQ	3514	1
905	GTGGTGGTG	2015	RSSALTR	2515	RSDSLAR	3015	RSDSLAR	3515	1.15
908	AAGGTCTCA	2016	QSGDLRT	2516	DRSALAR	3016	RSDNLRQ	3516	50
909	GTGGAAGAA	2017	QSGNLSR	2517	QSGNLQR	3017	RSDALAR	3517	16.4
910	ATGGAAGAT	2018	QSSNLAR	2518	QSGNLQR	3018	RSDALAQ	3518	0.03
911	ATGGGTGCA	2019	QSGSLTR	2519	QSSHLAR	3019	RSDALAQ	3519	0.91
912	TCAGAGGTG	2020	RSDSLAR	2520	RSDNLTR	3020	QSGDLRT	3520	0.135
914	CAGGAAAAG	2021	RSDNLTQ	2521	QSGNLR	3021	RSDNLRE	3521	1.26
915	CAGGAAAAG	2022	RSDNLRQ	2522	QSGNLR	3022	RSDNLRE	3522	45.15
916	GAGGAAGGA	2023	QSGHLAR	2523	QSGNLR	3023	RSDNLQR	3523	1.3
919	TCATAGTAG	2024	RSDNLTT	2524	RSDNLRT	3024	QSGDLRT	3524	250
920	GATGTGGTA	2025	QSSSLVR	2525	RSDSLAR	3025	TSANLSR	3525	4
921	AAGGTCTCA	2026	QSGDLRT	2526	DPGALVR	3026	RSDNLRQ	3526	11
922	AAGGTCTCA	2027	QSHDLTK	2527	DRSALAR	3027	RSDNLRQ	3527	4
923	AAGGTCTCA	2028	QSHDLTK	2528	DPGALVR	3028	RSDNLRQ	3528	2
926	GTGGTGGTG	2029	RSDALTR	2529	RSDSLAR	3029	RSDSLAR	3529	7.502
927	CAGGTTGAG	2030	RSDNLAR	2530	TSGSLTR	3030	RSDNLRE	3530	3.61
928	CAGGTTGAG	2031	RSDNLAR	2531	QSSALTR	3031	RSDNLRE	3531	25
929	CAGGTAGAT	2032	QSSNLAR	2532	QSATLAR	3032	RSDNLRE	3532	1.3
931	GAGGAAGAG	2033	RSDNLAR	2533	QSSNLVR	3033	RSDNLAR	3533	2
932	ATGGAAGGG	2034	RSDHLAR	2534	QSSNLVR	3034	RSDALRQ	3534	797
933	GACGAGGAA	2035	QSANLAR	2535	RSDNLAR	3035	DRSNLTR	3535	500
934	ATGGAAGAT	2036	QSSNLAR	2536	QSGNLQR	3036	RSDALTS	3536	0.07
935	ATGGGTGCA	2037	QSGSLTR	2537	QSSHLAR	3037	RSDALTS	3537	0.91
937	GTGGGGGCT	2038	QSSDLTR	2538	RSDHLTR	3038	RSDSLAR	3538	0.03
938	GTGGGGGCT	2039	QSSDLRR	2539	RSDHLTR	3039	RSDSLAR	3539	0.049
939	GGGGGCTGG	2040	RSDHLTT	2540	DRSHLAR	3040	RSDHLSK	3540	0.352
940	GGGGGCTGG	2041	RSDHLTK	2541	DRSHLAR	3041	RSDHLSK	3541	1.5
941	GGGGCTGGG	2042	RSDHLAR	2542	QSSDLRR	3042	RSDKLSR	3542	0.077
942	GGGGCTGGG	2043	RSDHLAR	2543	QSSDLRR	3043	RSDHLSK	3543	0.13
943	GGGGCTGGG	2044	RSDHLAR	2544	TSGELVR	3044	RSDKLSR	3544	0.067
944	GGGGCTGGG	2045	RSDHLAR	2545	TSGELVR	3045	RSDHLSK	3545	0.027
945	GGTGCGGTG	2046	RSDSLTR	2546	RADTLRR	3046	MSHHLSR	3546	0.027
946	GGTGCGGTG	2047	RSDSLTR	2547	RSDVLQR	3047	MSHHLSR	3547	0.027
947	GGTGCGGTG	2048	RSDSLTR	2548	RSEDLQR	3048	QSSHLAR	3548	0.013
948	GGTGCGGTG	2049	RSDSLTR	2549	RSDVLQR	3049	QSSHLAR	3549	0.017
962	GAGGCGGCA	2050	QSGSLTR	2550	RSEDLQR	3050	RSDNLAR	3550	0.015
963	GAGGCGGCA	2051	QSGSLTR	2551	RSDDLQR	3051	RSDNLAR	3551	0.015
964	GCGGCGGTG	2052	RSDALAR	2552	RSEDLQR	3052	RSDERKR	3552	0.041

965	GCGGCGGCC	2053	ERGDLTR 2553	RSDELQR 3053	RSDEKRR 3553	3.1
966	GAGGAGGCC	2054	ERGTLLAR 2554	RSDNLSR 3054	RSDNLAR 3554	0.028
967	GAGGAGGCC	2055	DRSSLTR 2555	RSDNLSR 3055	RSDNLAR 3555	0.055
968	GAGGCCGCA	2056	QSGSLTR 2556	DRSSLTR 3056	RSDNLAR 3556	1.4
969	GAGGCCGCA	2057	QSGSLTR 2557	DRSDLTR 3057	RSDNLAR 3557	0.275
970	GTGGGCGCC	2058	ERGTLLAR 2558	DRSHLAR 3058	RSDALAR 3558	1.859
971	GTGGGCGCC	2059	DRSSLTR 2559	DRSHLAR 3059	RSDALAR 3559	0.144
972	GTGGGCGCC	2060	ERGDLTR 2560	DRSHLAR 3060	RSDALAR 3560	1.748
973	GCCGCGGTC	2061	DRSALTR 2561	RSDELQR 3061	ERGTLLAR 3561	0.6
974	GCCGCGGTC	2062	DRSALTR 2562	RSDELQR 3062	DRSDLTR 3562	0.038
975	CAGGCCGCT	2063	QSSDLTR 2563	DRSSLTR 3063	RSDNLRE 3563	1.1
976	CAGGCCGCT	2064	QSSDLTR 2564	DRSDLTR 3064	RSDNLRE 3564	4.12
977	CTGGCAGTG	2065	RSDSLTR 2565	QSGSLTR 3065	RSDALRE 3565	0.017
978	CTGGCAGTG	2066	RSDSLTR 2566	QSGDLTR 3066	RSDALRE 3566	1.576
979	CTGGCGGCG	2067	RSSDLTR 2567	RSDELQR 3067	RSDALRE 3567	1.59
980	CTGGCGGCG	2068	RSDDLTR 2568	RSDELQR 3068	RSDALRE 3568	2.2
981	CAGGCGGCG	2069	RSDDLTR 2569	RSDELQR 3069	RSDNLRE 3569	0.375
982	CCGGGCTGG	2070	RSDHLTT 2570	DRSHLAR 3070	RSDELRE 3570	0.03
983	CCGGGCTGG	2071	RSDHLTK 2571	DRSHLAR 3071	RSDELRE 3571	1.385
984	GACGGCGAG	2072	RSDNLAR 2572	DRSHLAR 3072	DRSNLTR 3572	1.6
985	GACGGCGAG	2073	RSDNLAR 2573	DRSHLAR 3073	EKANLTR 3573	0.965
986	GGTGCTGAT	2074	QSSNLQR 2574	QSSDLQR 3074	MSHHLSR 3574	1.6
987	GGTGCTGAT	2075	QSSNLQR 2575	QSSDLQR 3075	TSGHVLR 3575	33.55
988	GGTGCTGAT	2076	TSGNLVR 2576	QSSDLQR 3076	MSHHLSR 3576	0.15
989	GGTGAGGGG	2077	RSDHLAR 2577	RSDNLAR 3077	MSHHLSR 3577	1.9
990	AAGGTGGGC	2078	DRSHLTR 2578	RSDSLAR 3078	RSDNLTQ 3578	5.35
991	AAGGTGGGC	2079	DRSHLTR 2579	SSGSLVR 3079	RSDNLTQ 3579	0.06
993	GGGGCTGGG	2080	RSDHLAR 2580	TSSELVR 3080	RSDHLR 3580	3.1
994	GGGGCTGGG	2081	RSDHLTK 2581	DRSHLAR 3081	RSDHLR 3581	0.03
995	GGGGAGGAA	2082	QSANLAR 2582	RSDNLAR 3082	RSDHLR 3582	0.08
996	CAGTTGGTC	2083	DRSALAR 2583	RSDALTS 3083	RSDNLRE 3583	9.6
997	AGAGAGGCT	2084	QSSDLTR 2584	RSDNLAR 3084	QSGHLNQ 3584	1.65
998	ACGTAGTAG	2085	RSANLRT 2585	RSDNLTK 3085	RSDTLKQ 3585	0.23
999	AGAGAGGCT	2086	QSSDLTR 2586	RSDNLAR 3086	QSGKLTQ 3586	0.6
1000	CAGTTGGTC	2087	DRSALAR 2587	RSDALTR 3087	RSDNLRE 3587	11.15
1001	GGAGCTGAC	2088	EKANLTR 2588	QSSDLR 3088	QRAHLAR 3588	1.8
1002	GCGGAGGAG	2089	RSDNLVR 2589	RSDNLAR 3089	RSDEKRR 3589	0.028
1003	ACGTAGTAG	2090	RSANLRT 2590	RSDNLTK 3090	RSDTLRS 3590	0.118
1004	ACGTAGTAG	2091	RSDNLTT 2591	RSDNLTK 3091	RSDTLRS 3591	1.4
1006	GTAGGGGCG	2092	RSDDLTR 2592	RSDHLTR 3092	QRASLTR 3592	0.898
1007	GAGAGAGAT	2093	QSSNLQR 2593	QSGHLTR 3093	RLHNLAR 3593	167
1008	GAGATGGAG	2094	RSDNLSR 2594	RSDSLTQ 3094	RLHNLAR 3594	0.4
1009	GAGATGGAG	2095	RSDNLSR 2595	RSDSLTQ 3095	RSDNLSR 3595	1.9
1010	GAGAGAGAT	2096	QSSNLQR 2596	QSGHLTR 3096	RSDNLAR 3596	8.2
1011	TTGGTGGCG	2097	RSADLTR 2597	RSDSLAR 3097	RSDSLTK 3597	0.03
1012	GACGTAGGG	2098	RSDHLTR 2598	QSSSLVR 3098	DRSNLTR 3598	0.032
1013	GAGAGAGAT	2099	QSSNLQR 2599	QSGHLNQ 3099	RSDNLAR 3599	0.15

1014	GACGTAGGG	2100	RSDHLTR	2600	QSGSLTR	3100	DRSNLTR	3600	0.01
1015	GCGGAGGAG	2101	RSDNLVR	2601	RSDNLAR	3101	RSDTLKK	3601	0.008
1016	CAGTTGGTC	2102	DRSALAR	2602	RSDSLTK	3102	RSDNLRE	3602	0.09
1017	CTGGATGAC	2103	EKANLTR	2603	TSGNLVR	3103	RSDALRE	3603	0.233
1018	GTAGTAGAA	2104	QSANLAR	2604	QSSSLVR	3104	QRASLAR	3604	7.2
1019	AGGGAGGAG	2105	RSDNLAR	2605	RSDNLAR	3105	RSDHLTQ	3605	0.022
1020	ACGTAGTAG	2106	RSDNLTT	2606	RSDNLTK	3106	RSDTLKQ	3606	0.69
1022	GAGGAGGTG	2107	RSDALAR	2607	RSDNLAR	3107	RSDNLAR	3607	0.01
1024	GGGGAGGAA	2108	QSANLAR	2608	RSDNLAR	3108	RSDHLSR	3608	0.08
1025	GAGGAGGTG	2109	QSSALTR	2609	QSSSLVR	3109	RSDTLTQ	3609	0.115
1026	GTGGCTTGT	2110	MSHHLKE	2610	QSSDLR	3110	RSDALAR	3610	0.076
1027	GCGGCGGTG	2111	RSDALAR	2611	RSDELQR	3111	RSDELQR	3611	0.054
1032	GGTGCTGAT	2112	TSGNLVR	2612	QSSDLQR	3112	TSGHLVR	3612	0.52
1033	GTGTTCTGT	2113	RSDALAR	2613	DRSALT	3113	RSDALAR	3613	685.2
1034	GTGTTCTGT	2114	RSDALAR	2614	DRSALT	3114	RSDALAR	3614	14.55
1035	GTGTTCTGT	2115	RSDALAR	2615	DRSALT	3115	RSDALAR	3615	56
1037	GTAGGGGCA	2116	QSGSLTR	2616	RSDHLSR	3116	QRASLAR	3616	0.05
1038	GTAGGGGCA	2117	QTGELRR	2617	RSDHLSR	3117	QRASLAR	3617	0.152
1039	GGGGCTGGG	2118	RSDHLSR	2618	TSGELVR	3118	RSDHLTR	3618	1.37
1040	GGGGCTGGG	2119	RSDHLSR	2619	QSSDLQR	3119	RSDHLSK	3619	0.05
1041	TCATAGTAG	2120	RSDNLTT	2620	RSDNLRT	3120	QSHDLTK	3620	2.06
1043	CAGGGAGAG	2121	RSDNLAR	2621	QSGHLTR	3121	RSDNLRE	3621	0.16
1044	CAGGGAGAG	2122	RSDNLAR	2622	QRAHLER	3122	RSDNLRE	3622	1.07
1045	GGGGCAGGA	2123	QSGHLAR	2623	QSGSLTR	3123	RSDHLSR	3623	0.15
1046	GGGGCAGGA	2124	QSGHLAR	2624	QSGDLRR	3124	RSDHLSR	3624	0.09
1047	GGGGCAGGA	2125	QRAHLER	2625	QSGSLTR	3125	RSDHLSR	3625	24.7
1048	CAGGCTGTA	2126	QSGALTR	2626	QSSDLQR	3126	RSDNLRE	3626	1.387
1049	CAGGCTGTA	2127	QRASLAR	2627	QSSDLQR	3127	RSDNLRE	3627	55.6
1050	CAGGCTGTA	2128	QSSSLVR	2628	QSSDLQR	3128	RSDNLRE	3628	0.125
1051	GAGGCTGAG	2129	RSDNLTR	2629	QSSDLQR	3129	RSDNLVR	3629	0.02
1052	TAGGACGGG	2130	RSDHLAR	2630	EKANLTR	3130	RSDNLTT	3630	0.28
1053	TAGGACGGG	2131	RSDHLAR	2631	DRSNLTR	3131	RSDNLTT	3631	0.025
1054	GCTGCAGGG	2132	RSDHLAR	2632	QSGSLTR	3132	QSSDLQR	3632	0.033
1055	GCTGCAGGG	2133	RSDHLAR	2633	QSGSLTR	3133	TSGDLTR	3633	18.73
1056	GCTGCAGGG	2134	RSDHLAR	2634	QSGSLTR	3134	QSSDLQR	3634	0.045
1057	GCTGCAGGG	2135	RSDHLAR	2635	QSGDLTR	3135	TSGDLTR	3635	0.483
1058	GGGGCCGCG	2136	RSDELTR	2636	DRSSLTR	3136	RSDHLSR	3636	6.277
1059	GGGGCCGCG	2137	RSDELTR	2637	DRSDLTR	3137	RSDHLSR	3637	0.152
1060	GCGGAGGCC	2138	ERGTAR	2638	RSDNLAR	3138	RSDEKR	3638	0.69
1061	GTTGCGGGG	2139	RSDHLAR	2639	RSDELQR	3139	QSSALTR	3639	0.165
1062	GTTGCGGGG	2140	RSDHLAR	2640	RSDELQR	3140	TSGSLTR	3640	0.068
1063	GTTGCGGGG	2141	RSDHLAR	2641	RSDELQR	3141	MSHALSR	3641	0.96
1064	GCGGCAGTG	2142	RSDALTR	2642	QSGSLTR	3142	RSDEKR	3642	0.453
1065	TGGGGCGGG	2143	RSDHLAR	2643	DRSHLAR	3143	RSDHLTT	3643	1.37
1066	GAGGGCGGT	2144	QSSHLTR	2644	DRSHLAR	3144	RSDNLVR	3644	0.15
1067	GAGGGCGGT	2145	TSGHLVR	2645	DRSHLAR	3145	RSDNLVR	3645	1.37
1068	GCAGGGGGC	2146	DRSHLTR	2646	RSDHLTR	3146	QSGDLTR	3646	2.05

1069	GCAGGCGGT	2147	DRSHLTR	2647	RSDHLTR	3147	QSGSLTR	3647	0.1
1070	GGGGCAGGC	2148	DRSHLTR	2648	QSGSLTR	3148	RSDHLSR	3648	0.456
1071	GGGGCAGGC	2149	DRSHLTR	2649	QSGDLTR	3149	RSDHLSR	3649	0.2
1072	GGATTGGCT	2150	QSSDLTR	2650	RSDALTT	3150	QRAHLAR	3650	0.46
1073	GGATTGGCT	2151	QSSDLTR	2651	RSDALTK	3151	QRAHLAR	3651	1.37
1075	GTGTTGGCG	2152	RSDELTR	2652	RSDALTK	3152	RSDALTR	3652	0.915
1076	GCGGCAGCG	2153	RSDELTR	2653	QSGSLTR	3153	RSDEKTR	3653	4.1
1077	GCGGCAGCG	2154	RSDELTR	2654	QSGDLRR	3154	RSDEKTR	3654	6.2
1078	GGGGGGGCC	2155	ERGTLAR	2655	RSDHLSR	3155	RSDHLSR	3655	0.2
1079	GGGGGGGCC	2156	ERGDLTR	2656	RSDHLSR	3156	RSDHLSR	3656	4.1
1080	CTGGAGGCG	2157	RSDELTR	2657	RSDNLAR	3157	RSDALRE	3657	1.37
1081	GGGGAGGTG	2158	RSDALTR	2658	RSDNLTR	3158	RSDHLSR	3658	0.05
1082	CTGGCGGCG	2159	RSDELTR	2659	RSDELTR	3159	RSDALRE	3659	0.152
1083	CTGGTGGCA	2160	QSGDLTR	2660	RSDALSR	3160	RSDALRE	3660	0.152
1084	GGTGAGGCG	2161	RSDELTR	2661	RSDNLAR	3161	MSHHLR	3661	0.5
1085	GGTGAGGCG	2162	RSDELTR	2662	RSDNLAR	3162	QSSHLAR	3662	0.46
1086	GGGGCTGGG	2163	RSDHLSR	2663	QSSDLQR	3163	RSDHLTR	3663	0.1
1087	CGGGCGGCC	2164	ERGDLTR	2664	RSDELQR	3164	RSDHLAE	3664	1.24
1088	CGGGCGGCC	2165	ERGDLTR	2665	RSDELQR	3165	RSDHLRE	3665	0.905
1089	GACGAGGCT	2166	QSSDLRR	2666	RSDNLAR	3166	DRSNLTR	3666	0.171
1090	AAGGCGCTG	2167	RSDALRE	2667	RSDELQR	3167	RSDNLTR	3667	30.3
1091	GTAGAGGAC	2168	DRSNLTR	2668	RSDNLAR	3168	QRASLAR	3668	0.085
1092	GCCTTGGCT	2169	QSSDLRR	2669	RGDALTS	3169	DRSDLTR	3669	2.735
1093	GCGGAGTCG	2170	RSADLRT	2670	RSDNLAR	3170	RSDEKTR	3670	0.046
1094	GCGGTTGGT	2171	TSGHLVR	2671	QSSALTR	3171	RSDEKTR	3671	12.34
1095	GGGGGAGCC	2172	ERGDLTR	2672	QRAHLER	3172	RSDHLSR	3672	0.395
1096	GGGGGAGCC	2173	DRSSLTR	2673	QRAHLER	3173	RSDHLSR	3673	0.019
1097	GAGGCCGAA	2174	QSANLAR	2674	DCRDLAR	3174	RSDNLAR	3674	0.77
1098	GCCGGGGAG	2175	RSDNLTR	2675	RSDHLTR	3175	DRSDLTR	3675	0.055
1099	GCGGAGTCG	2176	TSGHLVR	2676	TSGSLTR	3176	RSDEKTR	3676	0.45
1100	GTGTTGGTA	2177	QSGALTR	2677	RGDALTS	3177	RSDALTR	3677	1.4
1101	ATGGGAGTT	2178	TTSALTR	2678	QRAHLER	3178	RSDALRQ	3678	0.065
1102	AAGGCAGAA	2179	QSANLAR	2679	QSGSLTR	3179	RSDNLTR	3679	8.15
1103	AAGGCAGAA	2180	QSANLAR	2680	QSGDLTR	3180	RSDNLTR	3680	1.4
1104	CGGGCAGCT	2181	QSSDLRR	2681	QSGSLTR	3181	RSDHLRE	3681	0.08
1105	CTGGCAGCC	2182	ERGDLTR	2682	QSGDLTR	3182	RSDALRE	3682	2.45
1106	CTGGCAGCC	2183	DRSSLTR	2683	QSGDLTR	3183	RSDALRE	3683	0.19
1107	GCGGGAGTT	2184	QSSALAR	2684	QRAHLER	3184	RSDEKTR	3684	0.06
1108	CAGGCTGGA	2185	QSGHLAR	2685	TSGELVR	3185	RSDNLRE	3685	0.007
1109	AGGGGAGCC	2186	ERGDLTR	2686	QRAHLER	3186	RSDHLTR	3686	0.347
1110	AGGGGAGCC	2187	DRSSLTR	2687	QRAHLER	3187	RSDHLTR	3687	0.095
1111	CTGGTAGGG	2188	RSDHLAR	2688	QSSSLVR	3188	RSDALRE	3688	0.095
1112	CTGGTAGGG	2189	RSDHLAR	2689	QSATLAR	3189	RSDALRE	3689	0.125
1113	CTGGGGGCA	2190	QSGDLTR	2690	RSDHLTR	3190	RSDALRE	3690	0.06
1114	CAGGTTGAT	2191	QSSNLAR	2691	TSGSLTR	3191	RSDNLRE	3691	2.75
1115	CAGGTTGAT	2192	QSSNLAR	2692	QSSALTR	3192	RSDNLRE	3692	0.7
1116	CCGGAAGCG	2193	RSDELTR	2693	QSSNLVR	3193	RSDELRE	3693	12.3

1117	GCAGCGCAG	2194	RSSNLRE	2694	RSDELTR	3194	QSGSLTR	3694	2.85
1118	TAGGGAGTC	2195	DRSALTR	2695	QRAHLER	3195	RSDNLTT	3695	1.4
1119	TGGGAGGGT	2196	TSGHLVR	2696	RSDNLAR	3196	RSDHLTT	3696	0.1
1120	AGGGACGCG	2197	RSDELTR	2697	DRSNLTR	3197	RSDHLTQ	3697	2.735
1121	CTGGTGGCC	2198	ERGDLTR	2698	RSDALTR	3198	RSDALRE	3698	2.76
1122	CTGGTGGCC	2199	DRSSLTR	2699	RSDALTR	3199	RSDALRE	3699	0.101
1123	TAGGAAGCA	2200	QSGSLTR	2700	QSGNLAR	3200	RSDNLTT	3700	0.065
1124	GTGGATGGA	2201	QSGHLAR	2701	TSGNLVR	3201	RSDALTR	3701	0.101
1126	TTGGCTATG	2202	RSDALTS	2702	TSGELVR	3202	RGDALTS	3702	0.46
1127	CAGGGGGTT	2203	QSSALAR	2703	RSDHLTR	3203	RSDNLRE	3703	0.1
1128	AAGGTCGCC	2204	ERGDLTR	2704	DPGALVR	3204	RSDNLTQ	3704	5.45
1130	GGTGCAGAC	2205	DRSNLTR	2705	QSGDLTR	3205	MSHHLR	3705	0.1
1131	GTGGGAGCC	2206	ERGDLTR	2706	QRAHLER	3206	RSDALTR	3706	0.95
1132	GGGGCTGGA	2207	QSGHLAR	2707	TSGELVR	3207	RSDHLR	3707	0.055
1133	GGGGCTGGA	2208	QRAHLER	2708	TSGELVR	3208	RSDHLR	3708	0.5
1134	TGGGGGTGG	2209	RSDHLTT	2709	RSDHLTR	3209	RSDHLTT	3709	0.067
1135	GCGGCGGGG	2210	RSDHLAR	2710	RSDELQR	3210	RSDEKR	3710	0.025
1136	CCGGGAGTG	2211	RSDALTR	2711	QRAHLER	3211	RSDTLRE	3711	0.225
1137	CCGGGAGTG	2212	RSSALTR	2712	QRAHLER	3212	RSDTLRE	3712	0.085
1138	CAGGGGGTA	2213	QSGALTR	2713	RSDHLTR	3213	RSDNLRE	3713	0.027
1139	ACGGCCGAG	2214	RSDNLAR	2714	DRSDLTR	3214	RSDTLTQ	3714	0.535
1140	AAGGGTGCG	2215	RSDELTR	2715	QSSHLAR	3215	RSDNLTQ	3715	0.3
1141	ATGGACTTG	2216	RGDALTS	2716	DRSNLTR	3216	RSDALTQ	3716	1.7
1148	TTGGAGGAG	2217	RSDNLTR	2717	RSDNLTR	3217	RGDALTS	3717	0.006
1149	TTGGAGGAG	2218	RSDNLTR	2718	RSDNLTR	3218	RSDALTK	3718	0.004
1150	GAAGAGGCA	2219	QSGSLTR	2719	RSDNLTR	3219	QSGNLTR	3719	0.004
1151	GTAGTATGG	2220	RSDHLTT	2720	QRSALAR	3220	QRASLAR	3720	1.63
1152	AAGGCTGGA	2221	QSGHLAR	2721	TSGELVR	3221	RSDNLTQ	3721	1.605
1153	AAGGCTGGA	2222	QRAHLAR	2722	TSGELVR	3222	RSDNLTQ	3722	8.2
1154	CTGGCGTAG	2223	RSDNLTT	2723	RSDELQR	3223	RSDALRE	3723	1.04
1156	ATGGTTGAA	2224	QSANLAR	2724	QSSALTR	3224	RSDALRQ	3724	7.2
1157	ATGGTTGAA	2225	QSANLAR	2725	TSGSLTR	3225	RSDALRQ	3725	0.885
1158	AGGGGAGAA	2226	QSANLAR	2726	QSGHLTR	3226	RSDHLTQ	3726	0.1
1159	AGGGGAGAA	2227	QSANLAR	2727	QRAHLER	3227	RSDHLTQ	3727	0.555
1160	TGGGAAGGC	2228	DRSHLAR	2728	QSSNLVR	3228	RSDHLTT	3728	0.415
1161	GAGGCCGGC	2229	DRSHLAR	2729	DRSDLTR	3229	RSDNLAR	3729	0.45
1162	GTGTTGGTA	2230	QSGALTR	2730	RADALMV	3230	RSDALTR	3730	0.465
1163	GTGTGAGCC	2231	ERGDLTR	2731	QSGHLTT	3231	RSDALTR	3731	1.45
1164	GTGTGAGCC	2232	ERGDLTR	2732	QSVHLQS	3232	RSDALTR	3732	15.4
1165	GCGAAGGTG	2233	RSDALTR	2733	RSDNLTQ	3233	RSDEKR	3733	1.4
1166	GCGAAGGTG	2234	RSDALTR	2734	RSDNLTQ	3234	RSSDRKR	3734	0.195
1167	GCGAAGGTG	2235	RSDALTR	2735	RSDNLTQ	3235	RSHDRKR	3735	0.95
1168	AAGGCGCTG	2236	RSDALRE	2736	RSSDLTR	3236	RSDNLTQ	3736	2.8
1169	GTAGAGGAC	2237	DRSNLTR	2737	RSDNLAR	3237	QSSSLVR	3737	0.053
1170	GCCTTGGCT	2238	QSSDLRR	2738	RADALMV	3238	DRSDLTR	3738	2.75
1171	GCGGAGTCG	2239	RSDDLRT	2739	RSDNLAR	3239	RSDEKR	3739	0.18
1172	GCCGGGGAG	2240	RSDNLTR	2740	RSDHLTR	3240	ERGDLTR	3740	0.01

1173	GCTGAAGGG	2241	RSDHLR	2741	QSGNLAR	3241	QSSDLRR	3741	0.008
1174	GCTGAAGGG	2242	RSDHLR	2742	QSSNLVR	3242	QSSDLRR	3742	0.018
1175	AAGGTCGCC	2243	DRSDLTR	2743	DPGALVR	3243	RSDNLQ	3743	8.9
1176	GTGGGAGCC	2244	DRSDLTR	2744	QRAHLER	3244	RSDALTR	3744	4.1
1177	CCGGGCGCA	2245	QSGSLTR	2745	DRSHLAR	3245	RSDTLRE	3745	4.1
1178	GAGGATGGC	2246	DRSHLAR	2746	TSGNLVR	3246	RSDNLAR	3746	0.085
1179	GCAGCGCAG	2247	RSSNLRE	2747	RSSDLTR	3247	QSGSLTR	3747	2.735
1180	AAGGAAAGA	2248	QSGHLNQ	2748	QSGNLAR	3248	RSDNLQ	3748	4.825
1181	TTGGCTATG	2249	RSDALRQ	2749	TSGELVR	3249	RGDALTS	3749	8.2
1182	CAGGAAGGC	2250	DRSHLAR	2750	QSGNLAR	3250	RSDNLRE	3750	1.48
1183	CAGGAAGGC	2251	DRSHLAR	2751	QSSNLVR	3251	RSDNLRE	3751	1.935
1184	AAGGAAAGA	2252	KNWKLQA	2752	QSGNLAR	3252	RSDNLQ	3752	2.785
1185	AAGGAAAGA	2253	KNWKLQA	2753	QSHNLAR	3253	RSDNLQ	3753	5.25
1186	GCCGAGGTG	2254	RSDSLLR	2754	RSKNLQR	3254	ERGTLAR	3754	27.5
1187	CTGGTGGGC	2255	DRSHLAR	2755	RSDALTR	3255	RSDALRE	3755	0.006
1188	GTAGTATGG	2256	RSDHLTT	2756	QSSSLVR	3256	QRASLAR	3756	2.74
1189	ATGGTTGAA	2257	QSANLAR	2757	TSGALTR	3257	RSDALRQ	3757	1.51
1190	ATGGCAGTG	2258	RSDALTR	2758	QSGDLTR	3258	RSDSLNQ	3758	1.484
1191	ATGGCAGTG	2259	RSDALTR	2759	QSGSLTR	3259	RSDSLNQ	3759	5.325
1192	ATGGCAGTG	2260	RSDALTR	2760	QSGDLTR	3260	RSDALTQ	3760	2.364
1193	ATGGCAGTG	2261	RSDALTR	2761	QSGSLTR	3261	RSDALTQ	3761	3.125
1194	GAGAAGGTG	2262	RSDALTR	2762	RSDNRTA	3262	RSDNLTR	3762	2.19
1195	GAGAAGGTG	2263	RSDALTR	2763	RSDNRTA	3263	RSSNLTR	3763	2.8
1197	GAAGGTGCC	2264	ERGDLTR	2764	MSHHLR	3264	QSGNLTR	3764	14.8
1199	ATGGAGAAG	2265	RSDNRTA	2765	RSDNLTR	3265	RSDALTQ	3765	3.428
1200	ATGGAGAAG	2266	RSDNRTA	2766	RSSNLTR	3266	RSDALTQ	3766	16.87
1201	ATGGAGAAG	2267	RSDNRTA	2767	RSHNLTR	3267	RSDALTQ	3767	14.8
1202	CTGGAGTAC	2268	DRSNLRT	2768	RSDNLTR	3268	RSDALRE	3768	2.834
1203	GGAGTACTG	2269	RSDALRE	2769	QRSALAR	3269	QRAHLAR	3769	2.945
1204	GGAGTACTG	2270	RSDALRE	2770	QSSSLVR	3270	QRAHLAR	3770	4.38
1205	CGGGCAGCT	2271	QSSDLRR	2771	QSGDLTR	3271	RSDHLRE	3771	0.9
1206	GCGGGAGTT	2272	TTSALTR	2772	QRAHLER	3272	RSDERKR	3772	0.034
1207	CAGGCTGGA	2273	QRAHLER	2773	TSGELVR	3273	RSDNLRE	3773	0.45
1209	CCGGAAGCG	2274	RSDELTR	2774	QSSNLVR	3274	RSDTLRE	3774	19.28
1211	GCAGCGCAG	2275	RSDNLRE	2775	RSDELTR	3275	QSGSLTR	3775	6.5
1212	CAGGGGGTT	2276	TTSALTR	2776	RSDHLTR	3276	RSDNLRE	3776	0.05
1213	GAAGAAGAG	2277	RSDNLTR	2777	QSSNLVR	3277	QSGNLTR	3777	12.3
1214	ATGGGAGTT	2278	TTSALTR	2778	QRAHLER	3278	RSDALTQ	3778	0.46
1215	GTGGGGGCT	2279	QSSDLRR	2779	RSDHLTR	3279	RSDALTR	3779	0.003
1217	GAAGAGGCA	2280	QSGSLTR	2780	RSDNLTR	3280	QSANLTR	3780	0.004
1218	GCGGTGAGG	2281	RSDHLTQ	2781	RSQALTR	3281	RSDERKR	3781	0.46
1219	AAGGAAAGG	2282	RSDHLTQ	2782	QSHNLAR	3282	RSDNLQ	3782	0.68
1220	AAGGAAAGG	2283	RSDHLTQ	2783	QSGNLAR	3283	RSDNLQ	3783	0.175
1221	AAGGAAAGG	2284	RSDHLTQ	2784	QSSNLVR	3284	RSDNLQ	3784	1.4
1222	CAGGAGGGC	2285	DRSHLAR	2785	RSDNLAR	3285	RSDNLRE	3785	0.155
1223	ATGGACTTG	2286	RSDALTK	2786	DRSNLTR	3286	RSDALTQ	3786	7
1224	ATGGACTTG	2287	RADALMV	2787	DRSNLTR	3287	RSDALTQ	3787	12

1227	GAATAGGGG	2288	RSDHLSR 2788	RSDHLTK 3288	QSGNLAR 3788	25
1228	ACGGCCGAG	2289	RSDNLAR 2789	DRSDLTR 3289	RSDDLQ 3789	12
1229	AAGGGTGCG	2290	RSDELTR 2790	MSHLSR 3290	RSDNLQ 3790	8.2
1230	AAGGGAGAC	2291	DRSNLTR 2791	QSGHLTR 3291	RSDNLQ 3791	0.383
1231	AAGGGAGAC	2292	DRSNLTR 2792	QRAHLER 3292	RSDNLQ 3792	0.213
1232	TGGGACCTG	2293	RSDALRE 2793	DRSNLTR 3293	RSDHLTT 3793	0.113
1233	TGGGACCTG	2294	RSDALRE 2794	DRSNLTR 3294	RSDHLTT 3794	0.635
1234	GAGTAGGCA	2295	QSGSLTR 2795	RSDNLTK 3295	RSDNLAR 3795	0.101
1236	GAGTAGGCA	2296	QSGSLTR 2796	RSDHLTT 3296	RSDNLAR 3796	0.065
1237	GAAGGAGAG	2297	RSDNLAR 2797	QRAHLER 3297	QSGNLAR 3797	0.065
1238	CTGGATGTT	2298	QSSALAR 2798	TSGNLVR 3298	RSDALRE 3798	0.313
1239	CAGGACGTG	2299	RSDALTR 2799	DPGNLVR 3299	RSDNLKD 3799	0.144
1240	GGGGAGGCA	2300	QSGSLTR 2800	RSDNLTR 3300	RSDHLSR 3800	0.056
1241	GAGGTGTCA	2301	QSHDLTK 2801	RSDALAR 3301	RSDNLAR 3801	0.027
1242	GGGGTTGAA	2302	QSANLAR 2802	TSGSLTR 3302	RSDHLSR 3802	0.02
1243	GGGGTTGAA	2303	QSANLAR 2803	QSSALTR 3303	RSDHLSR 3803	0.101
1244	GTCGCGGTG	2304	RSDALTR 2804	RSDELQR 3304	DRSALAR 3804	0.044
1245	GTCGCGGTG	2305	RSDALTR 2805	RSDELQR 3305	DSGSLTR 3805	0.102
1246	GTGGTTGCG	2306	RSDELTR 2806	TSGSLTR 3306	RSDALTR 3806	0.051
1247	GTGGTTGCG	2307	RSDELTR 2807	TSGALTR 3307	RSDALTR 3807	0.117
1248	GTCTAGGTA	2308	QSGALTR 2808	RSDNLTT 3308	DRSALAR 3808	5.14
1249	CCGGGAGCG	2309	RSDELTR 2809	QSGHLTR 3309	RSDTLRE 3809	0.26
1250	GAAGGAGAG	2310	RSDNLAR 2810	QSGHLTR 3310	QSGNLAR 3810	0.31
1252	CCGGCTGGA	2311	QRAHLER 2811	QSSDLTR 3311	RSDTLRE 3811	0.153
1253	CCGGGAGCG	2312	RSDELTR 2812	QRAHLER 3312	RSDTLRE 3812	0.228
1255	ACGTAGTAG	2313	RSDNLTT 2813	RSDNLTK 3313	RSDTLKQ 3813	0.69
1256	GGGGAGGAT	2314	QSSNLAR 2814	RSDNLQR 3314	RSDHLSR 3814	2
1257	GGGGAGGAT	2315	TTSNLAR 2815	RSDNLQR 3315	RSDHLSR 3815	1
1258	GGGGAGGAT	2316	QSSNLRR 2816	RSDNLQR 3316	RSDHLSR 3816	2
1259	GAGTGTGTG	2317	RSDSLLR 2817	DRDHLTR 3317	RSDNLAR 3817	1.5
1260	GAGTGTGTG	2318	RLDSLRL 2818	DRDHLTR 3318	RSDNLAR 3818	1.8
1261	TGCGGGGCA	2319	QSGDLTR 2819	RSDHLTR 3319	RRDTLHR 3819	0.2
1262	TGCGGGGCA	2320	QSGDLTR 2820	RSDHLTR 3320	RLDTLGR 3820	3
1263	TGCGGGGCA	2321	QSGDLTR 2821	RSDHLTR 3321	DSGHLAS 3821	21
1264	AAGTTGGTT	2322	TTSALTR 2822	RADALMV 3322	RSDNLQ 3822	0.21
1265	AAGTTGGTT	2323	TTSALTR 2823	RSDALTT 3323	RSDNLQ 3823	0.077
1266	CAGGGTGGC	2324	DRSHLTR 2824	QSSHLAR 3324	RSDNLRE 3824	6.1
1267	TAGGCAGTC	2325	DRSALTR 2825	QSGSLTR 3325	RSDNLTT 3825	6
1268	CTGTTGGCT	2326	QSSDLTR 2826	RADALMV 3326	RSDALRE 3826	1.52
1269	CTGTTGGCT	2327	QSSDLTR 2827	RSDALTT 3327	RSDALRE 3827	12.3
1270	TTGGATGGA	2328	QSGHLAR 2828	TSGNLVR 3328	RSDALTK 3828	0.4
1271	GTGGCACTG	2329	RSDALRE 2829	QSGSLTR 3329	RSDALTR 3829	0.915
1272	CAGGAGTCC	2330	DRSSLTT 2830	RSDNLAR 3330	RSDNLRE 3830	0.04
1273	CAGGAGTCC	2331	ERGDLT 2831	RSDNLAR 3331	RSDNLRE 3831	0.1
1274	GCATGGGAA	2332	QSANLSR 2832	RSDHLTT 3332	QSGSLTR 3832	0.306
1275	GCATGGGAA	2333	QRSNLVR 2833	RSDHLTT 3333	QSGSLTR 3833	0.326
1276	TAGGAAGAG	2334	RSDNLAR 2834	QRSNLVR 3334	RSDNLTT 3834	0.685

1277	GAAGAGGGG	2335	RSDHLAR	2835	RSDNLAR	3335	QSGNLTR	3835	0.421
1278	GAGTAGGCA	2336	QSGSLTR	2836	RSDNLRT	3336	RSDNLAR	3836	0.019
1279	GAGGTGTCA	2337	QSGDLRT	2837	RSDALAR	3337	RSDNLAR	3837	0.025
1282	TCGGTCGCC	2338	ERGDLTR	2838	DPGALVR	3338	RSDELRT	3838	74.1
1287	GTGGTAGGA	2339	QSGHLAR	2839	QSGALAR	3339	RSDALTR	3839	0.152
1288	CAGGGTGGC	2340	DRSHLTR	2840	QSSHLAR	3340	RSDNLTE	3840	4.1
1289	TAGGCAGTC	2341	DRSALTR	2841	QSGSLTR	3341	RSDNLTK	3841	1.37
1290	GTGGTGATA	2342	QSGALTQ	2842	RSHALTR	3342	RSDALTR	3842	24.05
1291	GTGGTGATA	2343	QQASLNA	2843	RSHALTR	3343	RSDALTR	3843	20.55
1292	TTGGATGGA	2344	QSGHLAR	2844	TSGNLVR	3344	RSDALTT	3844	4.12
1293	AAGGTAGGT	2345	TSGHLVR	2845	QSGALAR	3345	RSDNLTK	3845	0.457
1294	AAGGTAGGT	2346	MSHHLR	2846	QSGALAR	3346	RSDNLTK	3846	2.75
1295	CAGGAGTCC	2347	DRSSLTT	2847	RSDNLAR	3347	RSDNLTE	3847	0.116
1296	CAGGAGTCC	2348	ERGDLT	2848	RSDNLAR	3348	RSDNLTE	3848	37
1297	TAGGAAGAG	2349	RSDNLAR	2849	QRSNLVR	3349	RSDNLTK	3849	0.05
1298	CAGGACGTG	2350	RSDLATR	2850	DPGNLVR	3350	RSDNLTE	3850	0.05
1300	GTCTAGGTA	2351	QSGALTR	2851	RSDNLTK	3351	DRSALAR	3851	0.46
1302	CCGGCTGGA	2352	QSGHLTR	2852	QSSDLTR	3352	RSDTLRE	3852	0.05
1303	TAGGAGTTT	2353	QRSALAS	2853	RSDNLAR	3353	RSDNLTK	3853	0.088
1306	CTGGCCTTG	2354	RSDALTT	2854	DCRDLAR	3354	RSDALRE	3854	2.285
1308	TGGGCAGCC	2355	ERGTLAR	2855	QSGSLTR	3355	RSDHLTT	3855	0.305
1309	TAGGAGTTT	2356	QSSALAS	2856	RSDNLAR	3356	RSDNLTK	3856	0.184
1310	TAGGAGTTT	2357	TTSALAS	2857	RSDNLAR	3357	RSDNLTK	3857	0.075
1311	TGGGCAGCC	2358	ERGDLAR	2858	QSGSLTR	3358	RSDHLTT	3858	0.91
1312	GGGGCGTGA	2359	QSGHLTK	2859	RSDELQR	3359	RSDHLR	3859	0.23
1313	GGGGCGTGA	2360	QSGHLTT	2860	RSDELQR	3360	RSDHLR	3860	0.09
1314	GTACAGTAG	2361	RSDNLTK	2861	RSDNLRE	3361	QSSSLVR	3861	3.09
1315	GTACAGTAG	2362	RSDNLTK	2862	RSDNLTE	3362	QSSSLVR	3862	9.27
1318	ATGGTGTGT	2363	TSSHLAS	2863	RSDALAR	3363	RSDALAQ	3863	0.048
1319	ATGGTGTGT	2364	MSHHLTK	2864	RSDALAR	3364	RSDALAQ	3864	0.228
1320	TTGGGAGAG	2365	RSDNLAR	2865	QRAHLER	3365	RSDALTT	3865	0.044
1321	TTGGGAGAG	2366	RSDNLAR	2866	QRAHLER	3366	RADALMV	3866	0.127
1322	GTGGGAATA	2367	QSGALTQ	2867	QSGHLTR	3367	RSDALTR	3867	0.799
1323	GTGGGAATA	2368	QLTGLNQ	2868	QSGHLTR	3368	RSDALTR	3868	0.744
1324	GTGGGAATA	2369	QQASLNA	2869	QSHHLTR	3369	RSDALTR	3869	18.52
1325	TTGGTTGGT	2370	TSGHLVR	2870	TSGSLTR	3370	RSDALTK	3870	0.306
1326	TTGGTTGGT	2371	TSGHLVR	2871	QSSALTR	3371	RSDALTK	3871	4.385
1327	TTGGTTGGT	2372	TSGHLVR	2872	TSGSLTR	3372	RSDALTT	3872	0.566
1328	TTGGTTGGT	2373	TSGHLVR	2873	QSSALTR	3373	RSDALTT	3873	7.95
1329	CTGGCCTGG	2374	RSDHLTK	2874	DRSDLTR	3374	RSDALRE	3874	0.68
1330	GAGGTGTGA	2375	QSGHLTK	2875	RSDALTR	3375	RSDNLAR	3875	0.175
1331	CTGGCCTGG	2376	RSDHLTK	2876	DCRDLAR	3376	RSDALRE	3876	0.388
1334	CCGGCGCTG	2377	RSDALRE	2877	RSSDLTR	3377	RSDDLRE	3877	0.31
1335	GACGCTGGC	2378	DRSHLTR	2878	QSSDLTR	3378	DSSNLTR	3878	1.4
1336	CGGGCTGGA	2379	QSGHLAR	2879	QSSDLTR	3379	RSDHLAE	3879	1.4
1337	CGGGCTGGA	2380	QSSHLAR	2880	QSSDLTR	3380	RSDHLAE	3880	0.235
1338	GGGATGGCG	2381	RSDELTR	2881	RSDALTK	3381	RSDHLR	3881	1.04

1339	GGGATGGCG	2382	RSDELTR	2882	RSDSLTQ	3382	RSDHLSR	3882	0.569
1340	GGGATGGCG	2383	RSDELTR	2883	RSDALTQ	3383	RSHHLSR	3883	0.751
1341	GGGATGGCG	2384	RSDELTR	2884	RSDSLTQ	3384	RSHHLSR	3884	4.1
1342	CAGGCGCAG	2385	RSDNLRE	2885	RSSDLTR	3385	RSDNLTE	3885	0.68
1343	CAGGCGCAG	2386	RSDNLTT	2886	RTSTLTR	3386	RSDNLTE	3886	37.04
1344	CCGGGCGAC	2387	DRSNLTR	2887	DRSHLAR	3387	RSDTLRE	3887	2.28
1346	GATGTGTGA	2388	QSGHLTT	2888	RSDALAR	3388	TSANLSR	3888	0.153
1347	CAGTGAATG	2389	RSDALTS	2889	QSHHLTT	3389	RSDNLTE	3889	8.23
1348	GGGTCACTG	2390	RSDALTA	2890	QAATLTT	3390	RSDHLSR	3890	2.58
1350	CAGTGAATG	2391	RSDALTQ	2891	QSGHLTT	3391	RSDNLTE	3891	74.1
1351	GGGTCACTG	2392	RSDALRE	2892	QSHDLTK	3392	RSDHLSR	3892	0.234
1352	GTGTGGGTC	2393	DRSALAR	2893	RSDHLTT	3393	RSDALTR	3893	0.023
1353	CTGGCGAGA	2394	QSGHLNQ	2894	RSDELQR	3394	RSDALRE	3894	56.53
1354	CTGGCGAGA	2395	KNWKLQA	2895	RSDELQR	3395	RSDALRE	3895	20.85
1355	GCTTTGGCA	2396	QSGSLTR	2896	RSDALTT	3396	QSSDLTR	3896	0.172
1356	GCTTTGGCA	2397	QSGSLTR	2897	RADALMV	3397	QSSDLTR	3897	0.034
1357	GACTTGGTA	2398	QSSSLVR	2898	RSDALTT	3398	DRSNLTR	3898	0.032
1358	GACTTGGTA	2399	QSSSLVR	2899	RADALMV	3399	DRSNLTR	3899	0.05
1360	CAGTTGTGA	2400	QSGHLTT	2900	RADALMV	3400	RSDNLTE	3900	41.7
1361	AAGGAAAAA	2401	QKTNLDT	2901	QSGNLQR	3401	RSDNLTO	3901	0.835
1362	AAGGAAAAA	2402	QSGNLNQ	2902	QSGNLQR	3402	RSDNLTO	3902	0.332
1363	AAGGAAAAA	2403	QKTNLDT	2903	QRSNLVR	3403	RSDNLTO	3903	74.1
1364	ATGGGTGAA	2404	QSANLSR	2904	QSSHLAR	3404	RSDALAQ	3904	1.22
1365	ATGGGTGAA	2405	QRSNLVR	2905	QSSHLAR	3405	RSDALAQ	3905	0.152
1366	ATGGGTGAA	2406	QSANLSR	2906	TSGHLVR	3406	RSDALAQ	3906	22.63
1367	ATGGGTGAA	2407	QRSNLVR	2907	TSGHLVR	3407	RSDALAQ	3907	1.028
1368	CTGGGAGAT	2408	QSSNLAR	2908	QRAHLER	3408	RSDALRE	3908	0.051
1369	CTGGGAGAT	2409	QSSNLAR	2909	QSGHLTR	3409	RSDALRE	3909	0.227
1373	GTGGTGGGC	2410	DRSHLTR	2910	RSDALSR	3410	RSDALTR	3910	0.025
1374	CCGGCGGTG	2411	RSDALTR	2911	RSDELQR	3411	RSDELRE	3911	0.003
1375	CCGGCGGTG	2412	RSDALTR	2912	RSDDLQR	3412	RSDELRE	3912	0.008
1376	CCGGCGGTG	2413	RSDALTR	2913	RSDEKQR	3413	RSDELRE	3913	0.858
1377	CCGGCGGTG	2414	RSDALTR	2914	RSDELQR	3414	RSDDLRE	3914	0.012
1378	CCGGCGGTG	2415	RSDALTR	2915	RSDDLQR	3415	RSDDLRE	3915	0.012
1379	CCGGCGGTG	2416	RSDALTR	2916	RSDEKQR	3416	RSDDLRE	3916	0.25
1380	GCCGACGGT	2417	QSSHLTR	2917	DRSNLTR	3417	ERGDLTR	3917	0.076
1381	GCCGACGGT	2418	QSSHLTR	2918	DPGNLVR	3418	ERGDLTR	3918	0.23
1382	GCCGACGGT	2419	QSSHLTR	2919	DRSNLTR	3419	DCRDLAR	3919	3.1
1383	GCCGACGGT	2420	QSSHLTR	2920	DPGNLVR	3420	DCRDLAR	3920	1.74
1384	GGTGTGGGC	2421	DRSHLTR	2921	RSDALSR	3421	MSHHLSR	3921	0.013
1385	TGGGCAAGA	2422	QSGHLNQ	2922	QSGSLTR	3422	RSDHLTT	3922	0.229
1386	TGGGCAAGA	2423	ENWKLQA	2923	QSGSLTR	3423	RSDHLTT	3923	0.193
1389	CTGGCCTGG	2424	RSDHLTT	2924	DCRDLAR	3424	RSDALRE	3924	0.175
1393	TGGGAAGCT	2425	QSSDLRR	2925	QSGNLAR	3425	RSDHLTT	3925	0.1
1394	TGGGAAGCT	2426	QSSDLRR	2926	QSGNLAR	3426	RSDHLTK	3926	0.04
1395	GAAGAGGGA	2427	QSGHLQR	2927	RSDNLAR	3427	QSGNLAR	3927	0.025
1396	GAAGAGGGA	2428	QRAHLAR	2928	RSDNLAR	3428	QSGNLAR	3928	0.107

1397	GAAGAGGGA	2429	QSSHLAR	2929	RSDNLAR	3429	QSGNLAR	3929	0.14
1398	TAATGGGGG	2430	RSDHLSR	2930	RSDHLTT	3430	QSGNLRT	3930	0.065
1399	TGGGAGTGT	2431	TKQHLKT	2931	RSDNLAR	3431	RSDHLTT	3931	0.1
1400	CCGGGTGAG	2432	RSDNLAR	2932	QSSHLAR	3432	RSDDLRE	3932	0.371
1401	GAGTTGGCC	2433	ERGTLAR	2933	RADALMV	3433	RSDNLAR	3933	0.167
1402	CTGGAGTTG	2434	RGDALTS	2934	RSDNLAR	3434	RSDALRE	3934	0.15
1403	ATGGCAATG	2435	RSDALTQ	2935	QSGSLTR	3435	RSDALTQ	3935	0.07
1404	GAGGCAGGG	2436	RSDHLSR	2936	QSGSLTR	3436	RSDNLAR	3936	0.022
1405	GAGGCAGGG	2437	RSDHLSR	2937	QSGDLTR	3437	RSDNLAR	3937	0.045
1406	GAAGCGGAG	2438	RSDNLAR	2938	RSDELTR	3438	QSGNLAR	3938	0.025
1407	GCGGGCGCA	2439	QSGSLTR	2939	DRSHLAR	3439	RSDEKRR	3939	0.585
1408	CCGGCAGGG	2440	RSDHLSR	2940	QSGSLTR	3440	RSDELRE	3940	0.305
1409	CCGGCAGGG	2441	RSDHLSR	2941	QSGSLTR	3441	RSDDLRE	3941	0.153
1410	CCGGCGGCG	2442	RSDELTR	2942	RSDELQR	3442	RSDELRE	3942	0.814
1411	TGAGGCGAG	2443	RSDNLAR	2943	DRSHLAR	3443	QSGHLTK	3943	0.282
1412	CTGGCCGTG	2444	RSDSLLR	2944	ERGTLAR	3444	RSDALRE	3944	0.172
1413	CTGGCCGCG	2445	RSDELTR	2945	DRSDLTR	3445	RSDALRE	3945	0.152
1414	CTGGCCGCG	2446	RSDELTR	2946	ERGTLAR	3446	RSDALRE	3946	0.914
1415	GCGGCCGAG	2447	RSDNLAR	2947	DRSDLTR	3447	RSDELQR	3947	0.102
1416	GCGGCCGAG	2448	RSDNLAR	2948	ERGTLAR	3448	RSDELQR	3948	0.153
1417	GAGTTGGCC	2449	ERGTLAR	2949	RGDALTS	3449	RSDNLAR	3949	1.397
1418	CTGGAGTTG	2450	RADALMV	2950	RSDNLAR	3450	RSDALRE	3950	0.241
1422	GGGTCGGCG	2451	RSDELTR	2951	RSDDLTT	3451	RSDHLSR	3951	0.064
1423	GGGTCGGCG	2452	RSDELTR	2952	RSDDLTK	3452	RSDHLSR	3952	0.034
1424	CAGGGCCCG	2453	RSDELRE	2953	DRSHLAR	3453	RSDNLRE	3953	1.37
1427	CAGGGCCCG	2454	RSDDLRE	2954	DRSHLAR	3454	RSDNLTE	3954	0.271
1428	TGAGGCGAG	2455	RSDNLAR	2955	DRSHLAR	3455	QSVHLQS	3955	0.102
1429	TGAGGCGAG	2456	RSDNLAR	2956	DRSHLAR	3456	QSGHLTT	3956	0.074
1430	TCGGCCGCC	2457	ERGTLAR	2957	DRSDLTR	3457	RSDDLTK	3957	0.352
1431	TCGGCCGCC	2458	ERGTLAR	2958	DRSDLTR	3458	RSDDLAS	3958	6.17
1432	TCGGCCGCC	2459	ERGTLAR	2959	ERGTLAR	3459	RSDDLTK	3959	1.778
1434	CTGGCCGTG	2460	RSDSLLR	2960	DRSDLTR	3460	RSDALRE	3960	0.051
1435	TAATGGGGG	2461	RSDHLSR	2961	RSDHLTT	3461	QSGNLTK	3961	0.057
1436	TGGGAGTGT	2462	TSDHLAS	2962	RSDNLAR	3462	RSDHLTT	3962	0.026
1439	GGAGTGTTA	2463	QRSALAS	2963	RSDALAR	3463	QSGHLQR	3963	0.075
1440	GGAGTGTTA	2464	QSGALTK	2964	RSDALAR	3464	QSGHLQR	3964	0.035
1441	ATAGCTGGG	2465	RSDHLSR	2965	QSSDLTR	3465	QSGALTQ	3965	0.262
1442	TGCTGGGCC	2466	ERGTLAR	2966	RSDHLTT	3466	DRSHLTK	3966	0.36
1443	TGGAAGGAA	2467	QSGNLAR	2967	RSDNLTK	3467	RSHHLTT	3967	0.22
1444	TGGAAGGAA	2468	QSGNLAR	2968	RSDNLTK	3468	RSHHLTT	3968	0.09
1445	TGGAAGGAA	2469	QSGNLAR	2969	RLDNLTA	3469	RSHHLTT	3969	0.182
1446	TGGAAGGAA	2470	QSGNLAR	2970	RLDNLTA	3470	RSHHLTT	3970	0.42
1454	GGAGAGGCT	2471	QSSDLRR	2971	RSDNLAR	3471	QSGHLQR	3971	0.01
1455	CGGGATGAA	2472	QSANLSR	2972	TSGNLVR	3472	RSDHLRE	3972	0.043
1456	GGAGAGGCT	2473	QSSDLRR	2973	RSDNLAR	3473	QRAHLAR	3973	0.016
1457	GCAGAGGAA	2474	QSANLSR	2974	RSDNLAR	3474	QSGSLTR	3974	0.014
1460	TTGGGGGAG	2475	RSDNLAR	2975	RSDHLTR	3475	RADALMV	3975	0.007

1461	GACGAGGAG	2476	RSANLAR	2976	RSDNLTR	3476	DRSNLTR	3976	0.014
1462	CGGGATGAA	2477	QSGNLAR	2977	TSGNLVR	3477	RSDHLRE	3977	0.05
1463	GAGGCTGTT	2478	TTSALTR	2978	QSSDLTR	3478	RSDNLAR	3978	0.003
1464	GACGAGGAG	2479	RSDNLAR	2979	RSDNLTR	3479	DRSNLTR	3979	0.002
1465	CTGGGAGTT	2480	TTSALTR	2980	QSGHLQR	3480	RSDALRE	3980	0.018
1466	CTGGGAGTT	2481	NRATLAR	2981	QSGHLQR	3481	RSDALRE	3981	0.017
1468	GGTGATGTC	2482	DRSALTR	2982	TSGNLVR	3482	MSHHLR	3982	0.08
1469	GGTGATGTC	2483	DRSALTR	2983	TSGNLVR	3483	TSGHLVR	3983	0.28
1470	GGTGATGTC	2484	DRSALTR	2984	TSGNLVR	3484	QRAHLR	3984	0.156
1471	CTGGTTGGG	2485	RSDHLR	2985	QSSALTR	3485	RSDALRE	3985	0.09
1472	TTGAAGGTT	2486	TTSALTR	2986	RSDNLQ	3486	RADALMV	3986	3.22
1473	TTGAAGGTT	2487	TTSALTR	2987	RSDNLQ	3487	RSDSLTT	3987	0.47
1474	TTGAAGGTT	2488	QSSALAR	2988	RSDNLQ	3488	RADALMV	3988	1.39
1475	TTGAAGGTT	2489	QSSALAR	2989	RSDNLQ	3489	RLHSLTT	3989	0.39
1476	TTGAAGGTT	2490	QSSALAR	2990	RSDNLQ	3490	RSDSLTT	3990	0.305
1477	GCAGCCCGG	2491	RSDHLRE	2991	DRSDLTR	3491	QSGSLTR	3991	2.31
1479	GAAAGTTCA	2492	QSHDLTK	2992	MSHHLQ	3492	QSGNLAR	3992	37.04
1480	GAAAGTTCA	2493	NKTDLGK	2993	TSGHLVQ	3493	QSGNLAR	3993	62.5
1481	GAAAGTTCA	2494	NKTDLGK	2994	TSDHLAS	3494	RSDELRE	3994	37.04
1482	CCGTGTGAC	2495	DRSNLTR	2995	TSDHLAS	3495	RSDELRE	3995	111.1
1483	CCGTGTGAC	2496	DRSNLTR	2996	MSHHLTT	3496	RSDELRE	3996	20.8
1484	GAAGTGGTA	2497	QSSSLVR	2997	RSDALSR	3497	QSGNLAR	3997	0.01
1485	AAGTGAGCT	2498	QSSDLRR	2998	QSGHLTT	3498	RSDNLQ	3998	1.537
1486	GGGTTTGAC	2499	DRSNLTR	2999	TTSALAS	3499	RSDHLR	3999	0.085
1487	TTGAAGGTT	2500	TTSALTR	3000	RSDNLQ	3500	RLHSLTT	4000	0.188
1488	AAGTGGTAG	2501	QSSDLRR	3001	QSGHLTT	3501	RLDNRTQ	4001	5.64
1490	CTGGTTGGG	2502	RSDHLR	3002	TSGSLTR	3502	RSDALRE	4002	0.04
1491	AAGGGTTCA	2503	NKTDLGK	3003	DSSKLSR	3503	RLDNRTA	4003	4.12
1492	AAGTGGTAG	2504	RSDNLTT	3004	RSDHLTT	3504	RSDNLQ	4004	1.37
1493	AAGTGGTAG	2505	RSDNLTT	3005	RSDHLTT	3505	RLDNRTQ	4005	15.09
1494	GGGTTTGAC	2506	DRSNLTR	3006	QRSALAS	3506	RSDHLR	4006	0.255
1496	TTGGGGGAG	2507	RSDNLAR	3007	RSDHLTR	3507	RSDALTT	4007	0.065
1497	GAGGCTCTT	2508	QSSALAR	3008	QSSDLTR	3508	RSDNLAR	4008	0.007
1498	GAGGTTGAT	2509	QSSNLAR	3009	QSSALTR	3509	RSDNLAR	4009	0.101
1499	GAGGTTGAT	2510	QSSNLAR	3010	TSGALTR	3510	RSDNLAR	4010	0.02
1500	GCAGAGGAA	2511	QSGNLAR	3011	RSDNLAR	3511	QSGSLTR	4011	0.003
1522	GCAATGGGT	2512	TSGHLVR	3012	RSDALTQ	3512	QSGDLTR	4012	0.08

TABLE 6

TRIPLET (5'→3')	FINGER (N → C)		
	F1	F2	F3
AGG			RXDHXXQ
ATG			RXDAXXQ
CGG			RXDHXXE
GAA		QXGNXXR	
GAC	DXSNXXR		DXSNXXR
GAG	RXDNXXR	RXSNXXR RXDNXXR	RXDNXXR
GAT	QXSNXXR TXSNXXR TXGNXXR	TXGNXXR	
GCA	QXGSXXR	QXGDXXR	
GCC	EXGTXXR		
GCG	RXDEXXR	RXDEXXR	RXDEXXR RXDTXXK
GCT	QXSDXXR	TXGEXXR QXSDXXR	
GGA		QXGHXXR	QXAHXXR
GGC	DXSHXXR	DXSHXXR	
GGG	RXDHXXR	RXDHXXR	RXDHXXR RXDHXXK
GGT			TXGHXXR
GTA		QXGSXXR QXATXXR	
GTG	RXDAXXR RXDSXXR	RXDAXXR	RXDAXXR
TAG		RXDNXXT	
TCG	RXDDXXK		
TGT		TXDHXXS	